SUPPORTING INFORMATION

Weighted protein interaction network analysis of Frontotemporal Dementia.

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Table S4. Comparison of the enrichment results between gProfiler, Panther and Webgestalt. The per-mil of enrichment is calculated referring to the total amount of enriched terms and is color-coded in red. Missing semantic classes are highlighted in pink.

Table S5. Comparison between the enrichment of the FTD-PN-IIH connecting over 8 interactomes (29 nodes) and the Albinism network (79 nodes). The per-mil of enrichment is calculated referring to the total amount of enriched terms and is color-coded in red. Overlapping semantic classes are highlighted in pink. Semantic classes exclusive to albinism are highlighted in blue and the specific GO-BP terms are listed at the bottom of the table.

Table S6. Table containing the relevant semantic classes as indicated by the enrichment of the IIHs.

Table S7. List of protein-IDs indicating proteins from the FTD-PN that contribute to enrichment of DNA damage control, gene expression regulation and waste disposal both in W-PPI-NA and WGCNA. IIHs are color-coded in red.

Figure S1. Examples of entries removed from the imput data (old protein identifiers, non-human taxid, non-defined detection interaction method and/or Pubmed identifier).

Figure S2 to S27. IIHs with their surrounding interactors and degree of connectivity across the interacomes of multiple seeds. Any IIH could either be: i) a seed; ii) a 1st layer interactor or; iii) a 2nd layer interactor. Provided that only VCP was an IIH and a seed, any IIH was actually either a 1st or 2nd layer interactor. When the IIH was part of the 1st layer of the FTD network, then its surroundings would include: seed(s) (highlighted in green) + 1st layer neighbors present in the first layer of the network and connected directly to the seeds (highlighted in blue) + 2nd layer neighbors (highlighted in purple and for which the IIH would be the “seed”). When the IIH was part of the 2nd layer of the FTD network, then its surroundings would only include seed(s) (highlighted in green) + 1st layer neighbors

connected directly to the seeds (highlighted in blue). As in the latter case the IIH would not be a “seed” for any interactome, the nodes highlighted in purple are absent.

Figure S28 to S40. The graph reports the percentage of GO-BP terms as distributed in sub-classes inside each single semantic class.

Figure S41 to S44. Graphs showing the contribution of the interactome (1^{st} + 2^{nd} layers) of each seed towards the enrichment of specific semantic classes. The semantic classes are part of functional blocks indicating phase transition, development/proliferation of epthelium, DNA damage repair, protein localization. The gray bars indicate the weighted threshold for each single interactome. Points above that threshold are considered to highly contribute towards enrichment. Interactomes contributing to enrichment are indicated by the arrows.

Figure S45. Heatmap reporting the importance of each interactome towards enrichment of each specific semantic class. Red = high involvement; orange = mid-high involvement; yellow = mid-low involvement, and; white = low involvement.

File S1. ID conversion table

File S2. Enrichment – gProfiler – entire network

File S3. Enrichment – gProfiler – IIHs

Supporting Table 1

ID	Group Name	Members	Code
COIP	Co-immunoprecipitation	Co-immunoprecipitation	MI:0019
		Anti-bait coIP	MI:0006
		Anti-tag coIP	MI:0007
		Immunodepleted coimmunoprecipitation	MI:0858
APMS	Affinity Purification Mass Spectrometry	Pull Down	MI:0096
		Tandem Affinity Purification	MI:0676
		GST Pulldown	MI:0059
		Affinity Chromatography	MI:0004
		Affinity Technology	MI:0400
		Chromatography technology	MI:0091
		His pull down	MI:0061
		Interactome parallel affinity capture	MI:0963
E	Enzymatic Assay (Generic)	Enzymatic Assay	MI:0415
		Protein Kinase Assay	MI:0424
		Phosphatase Assay	MI:0434
		Fluorescence Phosphatase Assay	MI:1019
		Cleavage Assay	MI:0990
		In-gel kinase assay	MI:0423
		Protease assay	MI:0435
		Cleavage reaction	MI:0194
		Dephosphorylation reaction	MI:0203
		In gel phosphatase assay	MI:0514
		Polymerization	MI:0953
		Phosphotransferase assay	MI:0841
		Kinase scintillation proximity assay	MI:0425
SE	Enzymatic Assay (Specific)	Sumoylation reaction	MI:0566
		Deacetylase assay	MI:0406
		Neddylase assay	MI:1010
		Acetylation reaction	MI:0192
		Acetylase assay	MI:0889
UE	Enzymatic Assay (Specific)	Ubiquitination Reaction	MI:0220
		Ubiquitin Binding	MI:0443
		Ubiquitinase Assay	MI:0997
		Deubiquitinase assay	MI:0998
PA	Arrays	Protein Array	MI:0089
		Peptide Array	MI:0081
		Array technology	MI:0008
		Antibody array	MI:0078
FW	Far-Western-Blot	Far-Western-Blot	MI:0047
		Anti tag western blot	MI:0705
CO	Comigration	Comigration in gel electrophoresis	MI:0807
		Comigration in SDS-PAGE	MI:0808
		Comigration in nn denaturing gel elect.	MI:0404
		Blue Native page	MI:0276
		Electrophoresis Mobility Shift Assay	MI:0413
		Electrophoresis mobility based method	MI:0962
		Electrophoretic mobility supershift assay	MI:0412
DT	Display technology	Display Technology	MI:0034
		Phage Display	MI:0084
		T7 Phage Display	MI:0108
		Lambda Phage Display	MI:0066
		Filamentous Phage Display	MI:0048
		Bacterial Display	MI:0009
		Yeast display	MI:0115
CX	Cross-linking	Cross-linking	MI:0030
		Protein CX with Bifunctional Reagent	MI:0031
MS	Molecular Sieving	Molecular Sieving	MI:0071
FB	Filter Binding	Filter Binding	MI:0049
CS	Cosedimentation	Cosedimentation	MI:0027
		Cosedimentation in solution	MI:0028
		Cosedimentation through density gradient	MI:0029
ELISA	ELISA	ELISA	MI:0411
CIP	Chromatin IP	Chromatin IP Assay	MI:0402
GTP	GTP/GDP Exchange assay	GTP/GDP Exchange assay	MI:0949
		GTPase assay	MI:0419
LUM	Luminescence Based Mam Interactome Mapping	Luminescence Based Mam Interactome Mapping	MI:0729
PX	Proximity Ligation Assay	Proximity Ligation Assay	MI:0813
		Proximity-dependent biotin identification	MI:1314
		Amplified luminescent proximity homogeneous assay	MI:0905
CD	Circular Dichroism	Circular Dichroism	MI:0016
NMR	Nuclear Magnetic Resonance	Nuclear Magnetic Resonance	MI:0077
		Solid state nmr	MI:1104
X	X-ray cristallography	X-ray cristallography	MI:0114
		X-ray scattering	MI:0828
SPR	Surface Plasmon Resonance	Surface Plasmon Resonance	MI:0107
		Surface plasmon resonance array	MI:0921
FT	Fluorescence Technology	Fluorescence Technology	MI:0051
		Bimolecular Fluo. Complementation	MI:0809
		Fluorescence Correlation Spectroscopy	MI:0052
		Classical Fluorescence Spectroscopy	MI:0017
		Fluorescence Resonance Energy Transfer	MI:0055
		Fluorescence Polarization Spectroscopy	MI:0053
		Bioluminescence resonance energy transfer	MI:0012
		Homogeneous time resolved fluorescence	MI:0510
		Fluorescence recovery after photobleaching	MI:1016
LS	Light Scattering	Light Scattering	MI:0067
		Dynamic Light Scattering	MI:0038
CAL	Isothermal Tritation Calorimetry	Isothermal Tritation Calorimetry	MI:0065
MS	Mass Spectrometry	MS of complexes	MI:0069
		Detection by MS	MI:0941
I	Imaging Technique	Imaging Technique	MI:0428
		Atomic Force Microscopy	MI:0872
		Electron Microscopy	MI:0040
		Transmission Electron Microscopy	MI:0020
		Light Microscopy	MI:0426
		Electron Tomography	MI:0410
		Fluorescence Microscopy	MI:0416
		Confocal Microscopy	MI:0663
TWO	Two Hybrid	Two Hybrid	MI:0018
		Two Hybrid Array	MI:0397
		Two Hybrid Pooling Approach	MI:0398
		Two Hybrid Fragment pooling approach	MI:0399
		Two Hybrid Prey Pooling Approach	MI:1112
		Validated Two Hybrid	MI:1356
		Two hybrid fragment pooling approach	MI:0399
		Protein three hybrid	MI:0437
		Reverse two hybrid	MI:0726
REC	Reconstruction	Reverse RAS Recruitment System	MI:0097
		Mammalian P-P interaction Trap	MI:0231
		Protein Complementation Assay	MI:0090
		Ubiquitin Reconstruction	MI:0112
		Beta Lactamase Complementation	MI:0011
		Transcriptional complementation assay	MI:0232
		Gal4-vp16 complementation	MI:0728
		Split luciferase complementation	MI:1203
		Beta galactosidase complementation	MI:0010
		Split renilla luciferase complementation	MI:1037
		Dihydrofolate reductase reconstruction	MI:0111
		Lex-a dimerization assay	MI:0369
G	Genetic Inference	Genetic Inference	MI:0254
		Rna interference	MI:0256
BIOID	BioID	BioID	MI:1313
SB	Ligand Binding	Saturation Binding	MI:0440
		Competition Binding	MI:0405
DNA	Footprinting	Footprinting	MI:0417
		DNase I footprinting	MI:0606
		Enzymatic footprinting	MI:0605
		Antisense oligonucleotides	MI:1192
FACS	FACS	Fluorescence-activated cell sorting	MI:0054
SCI	SPA	Scintillation proximity assay	MI:0099
DNACX	DNA-RNA-Protein interaction	Nucleic acid uv cross-linking assay	MI:0430
		Methyltransferase assay	MI:0515
		Rna immunoprecipitation	MI:1017
TSB	TSB	thermal shift binding	MI:1235
MW	MW	molecular weight estimation by autoradiography	MI:0821
UNSPM	Unspecified	experimental interaction detection	MI:0045
		biochemical	MI:0401
		unspecified	MI:0686
		biophysical	MI:0013
		solid phase assay	MI:0892
		gene name synonym	MI:MOV34-34KD
		gene name synonym	MI:HRIHFB2281
		gene name synonym	MI:bK984G1.4
		gene name synonym	MI:52

Supporting Table 2

Against ALL		
ADHESION		%
adhesion	8	32.0
cell-cell	6	24.0
cell-substrate	5	20.0
adherens-junction	4	16.0
cell-matrix	2	8.0
total	**25**	**100**
CELL CYCLE		%
cell cycle	20	17.9
segregation/cytokinesis	21	18.8
mitotic phase transition	13	11.6
cytoskeleton	13	11.6
DNA - damage checkpoint	12	10.7
G1/S phase transition	9	8.0
enzymes	6	5.4
checkpoint	5	4.5
G2/M phase transition	4	3.6
DNA - damage checkpoint G1	4	3.6
ubiquitin-proteasome	4	3.6
DNA - damage checkpoint G2	1	0.9
total	**112**	**100.0**
CELL DEATH		%
cell death	34	37.4
oxidative stress	15	16.5
mitochondria	10	11.0
extrinsic apoptosis	10	11.0
enzymes	8	8.8
intrinsic apoptosis	5	5.5
signaling	5	5.5
DNA damage	3	3.3
ER stress	1	1.1
total	**91**	**100**
CHROMATIN		%
chromatin	10	21.7
telomers	13	28.3
histone - acetylation	8	17.4
histone	5	10.9
histone - methylation	4	8.7
histone ubiquitin	4	8.7
histone - phosphorylation	2	4.3
total	**46**	**100.0**
DEVELOPMENT		%
development	115	67.3
neuronal	15	8.8
brain	11	6.4
neuronal - axon	8	4.7
glia	6	3.5
cell projection	5	2.9
cell-proliferation	4	2.3
epith. cell-proliferation	5	2.9
stem cell-proliferation	2	1.2
total	**171**	**100**
DNA METABOLISM		%
metabolism	24	35.3
repair	18	26.5
DNA - damage checkpoint	12	17.6
damage	6	8.8
DNA - damage checkpoint G1	4	5.9
damage cell death	3	4.4
DNA - damage checkpoint G2	1	1.5
total	**68**	**100.0**
IMMUNE SYSTEM		%
immune system	25	16.0
cytokine	28	17.9
lymphocytes	26	16.7
leukocytes	19	12.2
interferon	16	10.3
interleukin	12	7.7
antigen presentation	10	6.4
innate	7	4.5
receptors	7	4.5
differentiation	4	2.6
chemokine	2	1.3
total	**156**	**100**
LOCALIZATION		%
localization	24	44.4
protein localization - nucleus	13	24.1
protein localization - membrane	10	18.5
protein localization - mitochondria	4	7.4
protein localization - ER	3	5.6
total	**54**	**100.0**

Against BRAIN ONLY		
ADHESION		%
adhesion	7	28.0
cell-cell	6	24.0
cell-substrate	3	12.0
adherens-junction	4	16.0
cell-matrix	2	8.0
total	**22**	**88**
CELL CYCLE		%
cell cycle	17	15.2
segregation/cytokinesis	15	13.4
mitotic phase transition	19	17.0
cytoskeleton	11	9.8
DNA - damage checkpoint	15	13.4
G1/S phase transition	0	0.0
enzymes	4	3.6
checkpoint	5	4.5
G2/M phase transition	0	0.0
DNA - damage checkpoint G1	0	0.0
ubiquitin-proteasome	0	0.0
DNA - damage checkpoint G2	0	0.0
total	**86**	**76.8**
CELL DEATH		%
cell death	29	31.9
oxidative stress	8	8.8
mitochondria	9	9.9
extrinsic apoptosis	10	11.0
enzymes	7	7.7
intrinsic apoptosis	5	5.5
signaling	4	4.4
DNA damage	2	2.2
ER stress	1	1.1
total	**75**	**82.4176**
CHROMATIN		%
chromatin	9	19.6
telomers	11	23.9
histone - acetylation	6	13.0
histone	4	8.7
histone - methylation	4	8.7
histone ubiquitin	3	6.5
histone - phosphorylation	2	4.3
total	**39**	**84.8**
DEVELOPMENT		%
development	93	54.4
neuronal	11	6.4
brain	8	4.7
neuronal - axon	6	3.5
glia	4	2.3
cell projection		0.0
cell-proliferation	4	2.3
epith. cell-proliferation	4	2.3
stem cell-proliferation	1	0.6
total	**131**	**76.6082**
DNA METABOLISM		%
metabolism	22	32.4
repair	12	17.6
DNA - damage checkpoint	15	22.1
damage	4	5.9
DNA - damage checkpoint G1		0.0
damage cell death	2	2.9
DNA - damage checkpoint G2		0.0
total	**55**	**80.9**
IMMUNE SYSTEM		%
immune system	22	14.1
cytokine	23	14.7
lymphocytes	23	14.7
leukocytes	19	12.2
interferon	13	8.3
interleukin	9	5.8
antigen presentation	10	6.4
innate	7	4.5
receptors	7	4.5
differentiation	4	2.6
chemokine		0.0
total	**137**	**87.8205**
LOCALIZATION		%
localization	28	51.9
protein localization - nucleus	7	13.0
protein localization - membrane	10	18.5
protein localization - mitochondria	4	7.4
protein localization - ER	3	5.6
total	**52**	**96.3**

RNA METABOLISM		%
RNA - metabolism	30	23.1
gene silencing	16	12.3
translation	13	10.0
RNA - splicing	12	9.2
transcription - pol II promoter	12	9.2
transcription	11	8.5
RNA stability	9	6.9
gene expression	7	5.4
transcription factors	6	4.6
RNA - localization	6	4.6
transcription - pol I promoter	5	3.8
RNA - poly(A)	3	2.3
total	**130**	**100.0**
SIGNALING		%
signaling	46	21.1
cytokine	28	12.8
hormone	20	9.2
MAPK	17	7.8
interferon	16	7.3
growth factor	12	5.5
interleukin	12	5.5
Wnt	11	5.0
toll-like	8	3.7
NFkappaB	7	3.2
TGF	5	2.3
Fc	5	2.3
ERBB	4	1.8
insulin	4	1.8
JNK	4	1.8
ERK	3	1.4
JUN	3	1.4
amine	2	0.9
TOR	2	0.9
chemokine	2	0.9
catenin	1	0.5
ephrin	1	0.5
hippo	1	0.5
integrin	1	0.5
neurotrophin	1	0.5
NOD	1	0.5
TRK	1	0.5
total	**218**	**100.0**
STRESS		%
stress	11	19.3
cell death	16	28.1
response to oxigen	8	14.0
response to radiation	8	14.0
oxidative stress	12	21.1
ER - stress	2	3.5
total	**57**	**100.0**
TRANSPORT		%
transport	43	32.8
nuclear transport	25	19.1
endocytosis	13	9.9
exocytosis	12	9.2
vesicle - transport	12	9.2
transport of organelles	7	5.3
transport synaptic	6	4.6
cytoskeleton - cell projection	5	3.8
ER - transport	3	2.3
cytoskeleton - based movement	3	2.3
Golgi -vesicle	1	0.8
transport of chromosomes	1	0.8
total	**131**	**100.0**
WASTE DISPOSAL-QC		%
ubiquitin-proteasome	34	50.0
autophagy	12	17.6
ubiquitin-proteasome - ER	7	10.3
UPR	6	8.8
cell cycle	4	5.9
histone ubiquitination	4	5.9
ubiquitin-proteasome - SCF	1	1.5
total	**68**	**100.0**

RNA METABOLISM		%
RNA - metabolism	28	21.5
gene silencing	10	7.7
translation	10	7.7
RNA - splicing	8	6.2
transcription - pol II promoter	9	6.9
transcription	10	7.7
RNA stability	7	5.4
gene expression	8	6.2
transcription factors	5	3.8
RNA - localization	6	4.6
transcription - pol I promoter	5	3.8
RNA - poly(A)	1	0.8
total	**107**	**82.3**
SIGNALING		%
signaling	42	19.3
cytokine	23	10.6
hormone	15	6.9
MAPK	17	7.8
interferon	13	6.0
growth factor	9	4.1
interleukin	9	4.1
Wnt	11	5.0
toll-like	6	2.8
NFkappaB	7	3.2
TGF	5	2.3
Fc	5	2.3
ERBB	4	1.8
insulin	2	0.9
JNK	3	1.4
ERK	3	1.4
JUN	3	1.4
amine		0.0
TOR		0.0
chemokine		0.0
catenin	1	0.5
ephrin	1	0.5
hippo		0.0
integrin		0.0
neurotrophin		0.0
NOD	1	0.5
TRK	1	0.5
STAT	4	1.8
total	**185**	**83.0**
STRESS		%
stress	10	17.5
cell death	9	15.8
response to oxigen	8	14.0
response to radiation	8	14.0
oxidative stress	11	19.3
ER - stress	2	3.5
total	**48**	**84.2**
TRANSPORT		%
transport	15	11.5
nuclear transport	19	14.5
endocytosis	8	6.1
exocytosis	6	4.6
vesicle - transport	9	6.9
transport of organelles	7	5.3
transport synaptic	4	3.1
cytoskeleton - cell projection	4	3.1
ER - transport	3	2.3
cytoskeleton - based movement	3	2.3
Golgi -vesicle		0.0
transport of chromosomes	1	0.8
total	**79**	**60.3**
WASTE DISPOSAL-QC		%
ubiquitin-proteasome	30	44.1
autophagy	10	14.7
ubiquitin-proteasome - ER	7	10.3
UPR	4	5.9
cell cycle		0.0
histone ubiquitination	3	4.4
ubiquitin-proteasome - SCF	1	1.5
total	**55**	**80.9**

Supporting Table 3

ALL GENOME	
semantic class	**#**
adhesion cell matrix	1
cell cycle	11
cell cycle-cell-proliferation	3
cell cycle - checkpoint	3
cell cycle - phase transition	11
cytoskeleton	1
cell death	14
cell death - intrinsic apoptosis	1
cell death - signaling	3
development	2
NA	
DNA - damage	1
DNA - damage cell death	1
DNA - damage checkpoint	12
DNA - metabolism	3
DNA - repair	1
ER - stress	1
NA	
gene expression	3
protein localization	10
protein localization - membrane	2
protein localization -nucleus	2
response to stimulus - radiation	2
RNA - metabolism	2
signaling	10
signaling - growth factor	2
stress	4
stress - oxidative	2
transcription	2
transcription - pol II promoter	1
translation	1
transport	3
transport - intracellular	13
ubiquitin-proteasome	6
ubiquitin-proteasome - ER	1
UPR	4
TOTAL	***139***

BRAIN ONLY	
semantic class	**#**
adhesion cell matrix	1
cell cycle	7
NA	
cell cycle - checkpoint	3
cell cycle - phase transition	11
cytoskeleton	1
cell death	6
cell death - intrinsic apoptosis	1
cell death - signaling	3
development	1
DEVELOPMENT cell-proliferation epithel.	3
DNA - damage	1
DNA - damage cell death	1
DNA - damage checkpoint	11
DNA - metabolism	1
DNA - repair	1
ER - stress	1
gene expres -gene silencing	4
gene expression	3
NA	
protein localization - membrane	2
NA	
response to stimulus - radiation	2
NA	
signaling	9
NA	
stress	4
stress - oxidative	1
NA	
NA	
translation	2
transport	1
transport - intracellular	6
ubiquitin-proteasome	1
ubiquitin-proteasome - ER	1
UPR	4
TOTAL	***93***

Supporting Table 4

G:PROFILER			PANTHER			WEBGESTALT		
semantic.group	**numb.**	**‰**	**semantic.group**	**numb.**	**‰**	**semantic.group**	**numb.**	**‰**
adhesion	8	4.3	adhesion	8	5.5	adhesion	4	2.3
adhesion adherens junction	4	2.2	#			adhesion adherens junction	1	0.6
adhesion cell cell	6	3.2	adhesion cell cell	5	3.5	adhesion cell cell	3	1.7
adhesion cell matrix	2	1.1	adhesion cell matrix	1	0.7	adhesion cell matrix	2	1.2
adhesion cell substrate	5	2.7	adhesion cell substrate	1	0.7	adhesion cell substrate	4	2.3
ageing	5	2.7	ageing	3	2.1	ageing	7	4.0
autophagy	12	6.5	autophagy	7	4.9	autophagy	7	4.0
cell cycle	20	10.8	cell cycle	18	12.5	cell cycle	18	10.4
cell cycle-cytoskeleton	13	7.0	cell cycle-cytoskeleton	5	3.5	cell cycle-cytoskeleton	19	11.0
cell cycle - checkpoint	5	2.7	cell cycle - checkpoint	5	3.5	cell cycle - checkpoint	5	2.9
cell cycle - enzyme	6	3.2	cell cycle - enzyme	4	2.8	cell cycle - enzyme	4	2.3
cell cycle - phase transition	26	14.1	cell cycle - phase transition	20	13.9	cell cycle - phase transition	9	5.2
cell cycle - segregation/cytokinesis	21	11.4	cell cycle - segregation/cytokinesis	14	9.7	cell cycle - segregation/cytokinesis	16	9.2
cell death	34	18.4	cell death	24	16.6	cell death	35	20.2
cell death - enzymes	8	4.3	cell death - enzymes	7	4.9	cell death - enzymes	5	2.9
cell death - ER stress	1	0.5	cell death - ER stress	1	0.7	cell death - ER stress	1	0.6
cell death - extrinsic apoptosis	10	5.4	cell death - extrinsic apoptosis	7	4.9	cell death - extrinsic apoptosis	5	2.9
cell death - intrinsic apoptosis	5	2.7	cell death - intrinsic apoptosis	5	3.5	cell death - intrinsic apoptosis	5	2.9
cell death - mitochondria	10	5.4	cell death - mitochondria	5	3.5	cell death - mitochondria	3	1.7
cell death - oxidative stress	15	8.1	cell death - oxidative stress	4	2.8	cell death - oxidative stress	1	0.6
cell death - signaling	5	2.7	cell death - signaling	4	2.8	cell death - signaling	4	2.3
chromatin	10	5.4	chromatin	10	6.9	chromatin	10	5.8
cytoskeleton	37	20.0	cytoskeleton	24	16.6	cytoskeleton	41	23.7
cytoskeleton - based movement	3	1.6	cytoskeleton - based movement	3	2.1	cytoskeleton - based movement	4	2.3
cytoskeleton - cell projection	5	2.7	cytoskeleton - cell projection	4	2.8	cytoskeleton - cell projection	5	2.9
development	115	62.3	development	102	70.7	development	144	83.2
development - brain	11	6.0	development - brain	10	6.9	development - brain	11	6.4
development - glia	5	2.7	development - glia	5	3.5	development - glia	4	2.3
development - neuronal	15	8.1	development - neuronal	12	8.3	development - neuronal	18	10.4
development - neuronal - axon	8	4.3	development - neuronal - axon	7	4.9	development - neuronal - axon	8	4.6
DEVELOPMENT cell-proliferation	4	2.2	DEVELOPMENT cell-proliferation	4	2.8	DEVELOPMENT cell-proliferation	4	2.3
DEVELOPMENT cell-proliferation epithel.	5	2.7	DEVELOPMENT cell-proliferation epithel.	4	2.8	DEVELOPMENT cell-proliferation epithel.	8	4.6
DEVELOPMENT cell-proliferation stem	2	1.1	DEVELOPMENT cell-proliferation stem	1	0.7	DEVELOPMENT cell-proliferation stem	1	0.6
DNA - damage	6	3.2	DNA - damage	5	3.5	DNA - damage	6	3.5
DNA - damage cell death	3	1.6	DNA - damage cell death	2	1.4	DNA - damage cell death	2	1.2
DNA - damage checkpoint	17	9.2	DNA - damage checkpoint	16	11.1	DNA - damage checkpoint	11	6.4
DNA - metabolism	24	13.0	DNA - metabolism	21	14.6	DNA - metabolism	24	13.9
DNA - repair	18	9.7	DNA - repair	12	8.3	DNA - repair	9	5.2
enzyme	45	24.4	enzyme	40	27.7	enzyme	52	30.1
ER	2	1.1	ER	1	0.7	ER	3	1.7
ER - stress	2	1.1	ER - stress	2	1.4	ER - stress	1	0.6
ER - transport	3	1.6	ER - transport	2	1.4	ER - transport	1	0.6
esocytosis	12	6.5	esocytosis	9	6.2	esocytosis	8	4.6
gene expres -gene silencing	16	8.7	gene expres -gene silencing	8	5.5	gene expres -gene silencing	4	2.3
gene expres -transcription factors	6	3.2	gene expres -transcription factors	5	3.5	gene expres -transcription factors	6	3.5
gene expression	7	3.8	gene expression	8	5.5	gene expression	8	4.6
general	163	88.3	general	158	109.6	general	145	83.8
Golgi	3	1.6	Golgi	1	0.7	Golgi	3	1.7
Golgi -vesicle	1	0.5	Golgi -vesicle	1	0.7	Golgi - vesicle	2	1.2
histone	5	2.7	histone	4	2.8	histone	4	2.3
histone - acetylation	8	4.3	histone - acetylation	5	3.5	histone - acetylation	8	4.6
histone - methylation	4	2.2	histone - methylation	2	1.4	histone - methylation	7	4.0
histone - phosphorylation	2	1.1	histone - phosphorylation	1	0.7	histone - phosphorylation	3	1.7
immune system	25	13.5	immune system	18	12.5	immune system	24	13.9
immune system-chemokine	2	1.1	immune system-chemokine	1	0.7	immune system-chemokine	2	1.2
immune system - antigen presentation	10	5.4	immune system - antigen presentation	10	6.9	immune system - antigen presentation	10	5.8
immune system - differentiation	4	2.2	immune system - differentiation	3	2.1	immune system - differentiation	5	2.9
immune system - innate	7	3.8	immune system - innate	8	5.5	immune system - innate	8	4.6
immune system - leukocytes	19	10.3	immune system - leukocytes	12	8.3	immune system - leukocytes	16	9.2
immune system - lymphocytes	26	14.1	immune system - lymphocytes	14	9.7	immune system - lymphocytes	31	17.9
immune system - receptors	7	3.8	immune system - receptors	7	4.9	immune system - receptors	7	4.0
#			#			ion	4	2.3
localization	29	15.7	localization	27	18.7	localization	24	13.9
localization- RNA	1	0.5	localization- RNA	1	0.7	localization- RNA	1	0.6
localization - vesicle	1	0.5	localization - vesicle	1	0.7	localization - vesicle	1	0.6
#			#			localization golgi	1	0.6
#			#			lysosome	1	0.6
membrane	7	3.8	membrane	7	4.9	membrane	4	2.3
metabolism	112	60.6	metabolism	85	58.9	metabolism	113	65.3
mitochondria	8	4.3	mitochondria	5	3.5	mitochondria	5	2.9
mitochondria - transport	5	2.7	mitochondria - transport	2	1.4	mitochondria - transport	4	2.3
motility	5	2.7	motility	4	2.8	motility	5	2.9
muscle	35	18.9	muscle	18	12.5	muscle	32	18.5
nucleus	3	1.6	nucleus	4	2.8	nucleus	3	1.7
organelle	11	6.0	organelle	8	5.5	organelle	10	5.8
organelle - transport	2	1.1	organelle - transport	2	1.4	organelle - transport	2	1.2
phagocytosis	1	0.5	phagocytosis	1	0.7	#		
physiology	21	11.4	physiology	22	15.3	physiology	26	15.0
#			#			protein localization - cytoskeleton	2	1.2
protein localization - ER	3	1.6	protein localization - ER	3	2.1	protein localization - ER	3	1.7
protein localization - membrane	10	5.4	protein localization - membrane	6	4.2	protein localization - membrane	8	4.6
protein localization - mitochondria	4	2.2	protein localization - mitochondria	2	1.4	#		
protein localization - nucleus	13	7.0	protein localization -nucleus	6	4.2	protein localization -nucleus	5	2.9
protein modification	27	14.6	protein modification	26	18.0	protein modification	24	13.9
protein modification - acetylation	11	6.0	protein modification - acetylation	6	4.2	protein modification - acetylation	9	5.2
protein modification - alkylation	3	1.6	protein modification - alkylation	2	1.4	protein modification - alkylation	2	1.2
protein modification - folding	3	1.6	protein modification - folding	2	1.4	protein modification - folding	6	3.5
protein modification - neddylation	3	1.6	#			protein modification - neddylation	3	1.7
protein modification - phosphorylation	16	8.7	protein modification - phosphorylation	16	11.1	protein modification - phosphorylation	16	9.2
protein modification - sumoylation	3	1.6	protein modification - sumoylation	2	1.4	protein modification - sumoylation	3	1.7
response to stimulus	76	41.1	response to stimulus	74	51.3	response to stimulus	74	42.8
response to stimulus - oxigen	8	4.3	response to stimulus - oxigen	8	5.5	response to stimulus - oxigen	6	3.5
response to stimulus - radiation	8	4.3	response to stimulus - radiation	8	5.5	response to stimulus - radiation	8	4.6
RNA - localization	5	2.7	RNA - localization	5	3.5	RNA - localization	4	2.3
RNA - metabolism	30	16.2	RNA - metabolism	25	17.3	RNA - metabolism	23	13.3
RNA - poly(A)	3	1.6	#			RNA - poly(A)	4	2.3
RNA - splicing	12	6.5	RNA - splicing	7	4.9	RNA - splicing	12	6.9
RNA metabolism - stability	9	4.9	RNA metabolism - stability	4	2.8	RNA metabolism - stability	8	4.6
signaling	46	24.9	signaling	41	28.4	signaling	44	25.4
signaling - amine	2	1.1	#			#		
signaling - catenin	1	0.5	signaling - catenin	1	0.7	#		
signaling - cytokine	28	15.2	signaling - cytokine	19	13.2	signaling - cytokine	26	15.0
signaling - ephrin	1	0.5	signaling - ephrin	1	0.7	#		
signaling - ERBB	4	2.2	signaling - ERBB	3	2.1	signaling - ERBB	3	1.7
signaling - ERK	3	1.6	signaling - ERK	2	1.4	signaling - ERK	4	2.3
signaling - growth factor	12	6.5	signaling - growth factor	11	7.6	signaling - growth factor	11	6.4
signaling - hippo	1	0.5	#			signaling - hippo	1	0.6
signaling - hormone	20	10.8	signaling - hormone	13	9.0	signaling - hormone	20	11.6
signaling - insulin	4	2.2	signaling - insulin	3	2.1	signaling - insulin	7	4.0
signaling - integrin	1	0.5	#			signaling - integrin	1	0.6
signaling - interferon	16	8.7	signaling - interferon	5	3.5	signaling - interferon	24	13.9
signaling - interleukin	12	6.5	signaling - interleukin	5	3.5	signaling - interleukin	29	16.8
signaling - JNK	4	2.2	signaling - JNK	4	2.8	signaling - JNK	4	2.3
signaling - MAPK	17	9.2	signaling - MAPK	13	9.0	signaling - MAPK	15	8.7
signaling - neurotrophin	1	0.5						
signaling - NFkappaB	7	3.8	signaling - NFkappaB	7	4.9	signaling - NFkappaB	8	4.6
signaling - NOD	1	0.5	signaling - NOD	1	0.7	signaling - NOD	4	2.3
#			#			signaling - Notch	1	0.6
#			#			signaling - RIG	1	0.6
signaling - TGF	5	2.7	signaling - TGF	5	3.5	signaling - TGF	4	2.3
signaling - toll-like	8	4.3	signaling - toll-like	4	2.8	signaling - toll-like	12	6.9
signaling - TOR	2	1.1	#			signaling - TOR	3	1.7
signaling - TRK	1	0.5	#			signaling - TRK	1	0.6
signaling - Wnt	11	6.0	signaling - Wnt	11	7.6	signaling - Wnt	7	4.0
signaling -Fc	5	2.7	signaling -Fc	5	3.5	#		
signaling -JUN	3	1.6	signaling -JUN	3	2.1	signaling -JUN	3	1.7
stress	11	6.0	stress	8	5.5	stress	10	5.8
stress - oxidative	12	6.5	stress - oxidative	11	7.6	stress - oxidative	5	2.9
synapse	2	1.1	synapse	2	1.4	synapse	4	2.3
synapse - transport	6	3.2	synapse - transport	1	0.7	synapse - transport	3	1.7
telomers	13	7.0	telomers	6	4.2	telomers	2	1.2
#			tranport - ion	1	0.7	tranport - ion	2	1.2
transcription	11	6.0	transcription	10	6.9	transcription	7	4.0
transcription - pol I promoter	5	2.7	transcription - pol I promoter	4	2.8	transcription - pol I promoter	4	2.3
transcription - pol II promoter	12	6.5	transcription - pol II promoter	9	6.2	transcription - pol II promoter	11	6.4
translation	13	7.0	translation	11	7.6	translation	12	6.9
transport	16	8.7	transport	13	9.0	transport	17	9.8
transport - chromosomes	1	0.5	#			transport - chromosomes	1	0.6
transport - endocytosis	12	6.5	transport - endocytosis	7	4.9	transport - endocytosis	11	6.4
transport - endocytosis - vesicle	1	0.5						
transport - intracellular	22	11.9	transport - intracellular	19	13.2	transport - intracellular	22	12.7
transport - nuclear	25	13.5	transport - nuclear	16	11.1	transport - nuclear	26	15.0
ubiquitin-proteasome	34	18.4	ubiquitin-proteasome	30	20.8	ubiquitin-proteasome	30	17.3
ubiquitin-proteasome - cell cycle	4	2.2	ubiquitin-proteasome - cell cycle	4	2.8	ubiquitin-proteasome - cell cycle	4	2.3
ubiquitin-proteasome - ER	7	3.8	ubiquitin-proteasome - ER	4	2.8	ubiquitin-proteasome - ER	2	1.2
ubiquitin-proteasome - histone	4	2.2	ubiquitin-proteasome - histone	1	0.7	ubiquitin-proteasome - histone	5	2.9
ubiquitin-proteasome - SCF	1	0.5	#			ubiquitin-proteasome - SCF	1	0.6
#			#			ubiquitin-proteasome - SMAD	1	0.6
#			#			ubiquitin-proteasome -ISG15	1	0.6
UPR	6	3.2	UPR	4	2.8	UPR	6	3.5
vesicle	3	1.6	vesicle	2	1.4	vesicle	1	0.6
#			#			vesicle - coating	1	0.6
vesicle - transport	8	4.3	vesicle - transport	6	4.2	vesicle - transport	7	4.0
virus	26	14.1	virus	17	11.8	virus	19	11.0
total	**1847**		**total**	**1442**		**total**	**1730**	
			NA	**25**		**NA**	**635**	

Supporting Table 5

FTD - 29 IIHs			ALBINISM - 79 proteins		
semantic.group	**numb.**	**‰**	**semantic.group**	**numb.**	**‰**
adhesion cell matrix	1	3.7			
cell cycle	11	40.6	#		
cell cycle - checkpoint	3	11.1	#		
cell cycle - phase transition	11	40.6	#		
cell cycle-cell-proliferation	3	11.1			
cell death	14	51.7	#		
cell death - intrinsic apoptosis	1	3.7	#		
cell death - signaling	3	11.1	#		
development	2	7.4	#		
DNA - damage	1	3.7	#		
DNA - damage cell death	1	3.7	#		
DNA - damage checkpoint	12	44.3	#		
DNA - metabolism	3	11.1	#		
DNA - repair	1	3.7	#		
#			endocytosis	1	22.7
enzyme	4	14.8	enzyme	1	22.7
gene expression	3	11.1	#		
general	60	221.4	general	7	159.1
metabolism	31	114.4	metabolism	1	22.7
mitochondria	1	3.7	#		
organelle	2	7.4	#		
#			pigment	10	227.3
physiology	1	3.7	#		
protein localization	10	36.9	protein localization	1	22.7
protein localization - membrane	2	7.4	#		
protein localization -nucleus	2	7.4	#		
protein modification	14	51.7	#		
protein modification - folding	1	3.7	#		
protein modification - phosphorylation	4	14.8	#		
response to stimulus	13	48.0	response to stimulus	6	136.4
response to stimulus - radiation	2	7.4	#		
RNA - metabolism	2	7.4	#		
signaling	10	36.9	signaling	8	181.8
signaling - growth factor	2	7.4	#		
stress	4	14.8	#		
stress - oxidative	2	7.4	#		
stress - ER	1	3.7	#		
transcription	2	7.4	#		
transcription - pol II promoter	1	3.7	#		
translation	1	3.7	#		
transport	3	11.1	transport	2	45.5
transport - intracellular	13	48.0	transport - intracellular	6	136.4
ubiquitin-proteasome	6	22.1	#		
ubiquitin-proteasome - ER	1	3.7	#		
#			vesicle - transport	1	22.7
UPR	4	14.8	#		
virus	2	7.4	#		
total	**271**		**total**	**44**	

GO:0042440	*pigment metabolic process*
GO:0006582	*melanin metabolic process*
GO:0043474	*pigment metabolic process involved in pigmentation*
GO:0048066	*developmental pigmentation*
GO:0043324	*pigment metabolic process involved in developmental pigmentation*
GO:0048069	*eye pigmentation*
GO:0042441	*eye pigment metabolic process*
GO:0046148	*pigment biosynthetic process*
GO:0006726	*eye pigment biosynthetic process*
GO:0042438	*melanin biosynthetic process*

Supporting Table 6

p-value	T	Q	Q&T	Q&T/Q	Q&T/T	term ID	t name	t depth	Semantic_Group	Functional_Group
4.84E-05	194	4152	78	0.019	0.402	GO:0007160	cell-matrix adhesion	5	cell-matrix	**cell-matrix adhesion** 78 unique proteins
1.23E-04	91	4152	44	0.011	0.484	GO:0001952	regulation of cell-matrix adhesion	5	cell-matrix	
2.80E-08	340	4152	131	0.032	0.385	GO:0050673	epithelial cell proliferation	4	cell-proliferation	**epithelial cell proliferation** 165 unique proteins
1.32E-06	84	4152	45	0.011	0.536	GO:0048145	regulation of fibroblast proliferation	5	cell-proliferation	
2.20E-06	85	4152	45	0.011	0.529	GO:0048144	fibroblast proliferation	4	cell-proliferation	
2.71E-06	282	4152	108	0.026	0.383	GO:0050678	regulation of epithelial cell proliferation	5	cell-proliferation	
8.68E-03	52	4152	27	0.007	0.519	GO:0048146	positive regulation of fibroblast proliferation	6	cell-proliferation	
2.32E-32	612	4152	274	0.066	0.448	GO:0070848	response to growth factor	5	signaling - growth factor	**growth factor signaling** 349 unique proteins
1.05E-30	589	4152	263	0.063	0.447	GO:0071363	cellular response to growth factor stimulus	6	signaling - growth factor	
1.02E-19	121	4152	78	0.019	0.645	GO:0007173	epidermal growth factor receptor signaling pathway	9	signaling - growth factor	
3.26E-10	78	4152	48	0.012	0.615	GO:0042058	regulation of epidermal growth factor receptor signaling pathway	7	signaling - growth factor	
1.64E-09	43	4152	32	0.008	0.744	GO:0042059	negative regulation of epidermal growth factor receptor signaling pathway	6	signaling - growth factor	
3.73E-09	92	4152	52	0.013	0.565	GO:0048010	vascular endothelial growth factor receptor signaling pathway	8	signaling - growth factor	
3.50E-08	31	4152	23	0.006	0.742	GO:0070849	response to epidermal growth factor	4	signaling - growth factor	
4.29E-06	27	4152	21	0.005	0.778	GO:0071364	cellular response to epidermal growth factor stimulus	7	signaling - growth factor	
4.45E-03	107	4152	46	0.011	0.43	GO:0008543	fibroblast growth factor receptor signaling pathway	8	signaling - growth factor	
5.06E-03	133	4152	54	0.013	0.406	GO:0044344	cellular response to fibroblast growth factor stimulus	7	signaling - growth factor	
1.05E-02	139	4152	55	0.013	0.396	GO:0071774	response to fibroblast growth factor	4	signaling - growth factor	
1.47E-02	226	4152	80	0.019	0.354	GO:0090287	regulation of cellular response to growth factor stimulus	4	signaling - growth factor	
7.26E-77	516	4152	313	0.075	0.607	GO:0044770	cell cycle phase transition	4	phase transition	**mitotic phase transition** 313 unique proteins
2.03E-76	490	4152	302	0.073	0.616	GO:0044772	mitotic cell cycle phase transition	5	phase transition	
1.04E-41	288	4152	175	0.042	0.608	GO:1901990	regulation of mitotic cell cycle phase transition	6	phase transition	
9.67E-41	309	4152	182	0.044	0.589	GO:1901987	regulation of cell cycle phase transition	6	phase transition	
1.10E-15	150	4152	84	0.02	0.56	GO:1901988	negative regulation of cell cycle phase transition	6	phase transition	
3.75E-15	139	4152	79	0.019	0.568	GO:1901991	negative regulation of mitotic cell cycle phase transition	7	phase transition	
2.86E-04	59	4152	32	0.008	0.542	GO:1901989	positive regulation of cell cycle phase transition	7	phase transition	
3.50E-04	54	4152	30	0.007	0.556	GO:1901992	positive regulation of mitotic cell cycle phase transition	7	phase transition	
9.14E-03	26	4152	17	0.004	0.654	GO:0010458	exit from mitosis	8	phase transition	
9.83E-03	44	4152	24	0.006	0.545	GO:0007091	metaphase/anaphase transition of mitotic cell cycle	3	phase transition	
1.68E-02	45	4152	24	0.006	0.533	GO:0044784	metaphase/anaphase transition of cell cycle	6	phase transition	
2.43E-02	43	4152	23	0.006	0.535	GO:0030071	regulation of mitotic metaphase/anaphase transition	3	phase transition	
4.01E-02	44	4152	23	0.006	0.523	GO:1902099	regulation of metaphase/anaphase transition of cell cycle	6	phase transition	
1.54E-34	225	4152	140	0.034	0.622	GO:0000082	G1/S transition of mitotic cell cycle	6	phase transition	**G1/S phase transition** 144 unique proteins
1.73E-34	235	4152	144	0.035	0.613	GO:0044843	cell cycle G1/S phase transition	5	phase transition	
1.15E-16	141	4152	82	0.02	0.582	GO:1902806	regulation of cell cycle G1/S phase transition	7	phase transition	
1.29E-16	131	4152	78	0.019	0.595	GO:2000045	regulation of G1/S transition of mitotic cell cycle	7	phase transition	
1.63E-11	91	4152	55	0.013	0.604	GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	8	phase transition	
2.26E-11	94	4152	56	0.013	0.596	GO:1902807	negative regulation of cell cycle G1/S phase transition	7	phase transition	
9.14E-03	26	4152	17	0.004	0.654	GO:0000083	regulation of transcription involved in G1/S transition of mitotic cell cycle	10	phase transition	
1.95E-02	27	4152	17	0.004	0.63	GO:1902808	positive regulation of cell cycle G1/S phase transition	8	phase transition	
3.70E-02	23	4152	15	0.004	0.652	GO:1900087	positive regulation of G1/S transition of mitotic cell cycle	8	phase transition	
3.89E-27	190	4152	116	0.028	0.611	GO:0044839	cell cycle G2/M phase transition	5	phase transition	**G2/M phase transition** 116 unique proteins
2.25E-25	181	4152	110	0.026	0.608	GO:0000086	G2/M transition of mitotic cell cycle	6	phase transition	
2.86E-04	59	4152	32	0.008	0.542	GO:1902749	regulation of cell cycle G2/M phase transition	7	phase transition	
5.30E-03	51	4152	27	0.007	0.529	GO:0010389	regulation of G2/M transition of mitotic cell cycle	7	phase transition	
4.96E-27	213	4152	125	0.03	0.587	GO:0000075	cell cycle checkpoint	4	checkpoint	**cell cycle checkpoint** 125 unique proteins
5.68E-17	145	4152	84	0.02	0.579	GO:0007093	mitotic cell cycle checkpoint	6	checkpoint	
5.55E-10	69	4152	44	0.011	0.638	GO:0044819	mitotic G1/S transition checkpoint	9	checkpoint	
3.61E-08	65	4152	40	0.01	0.615	GO:0072395	signal transduction involved in cell cycle checkpoint	7	checkpoint	
1.40E-07	62	4152	38	0.009	0.613	GO:0072413	signal transduction involved in mitotic cell cycle checkpoint	8	checkpoint	
3.45E-24	153	4152	97	0.023	0.634	GO:0031570	DNA integrity checkpoint	5	DNA damage checkpoint	**DNA damage checkpoint** 125 unique proteins
9.73E-23	143	4152	91	0.022	0.636	GO:0000077	DNA damage checkpoint	6	DNA damage checkpoint	
9.45E-19	105	4152	70	0.017	0.667	GO:0030330	DNA damage response, signal transduction by p53 class mediator	7	DNA damage checkpoint	
1.19E-14	98	4152	62	0.015	0.633	GO:0044774	mitotic DNA integrity checkpoint	7	DNA damage checkpoint	
1.81E-13	92	4152	58	0.014	0.63	GO:0044773	mitotic DNA damage checkpoint	8	DNA damage checkpoint	
1.77E-08	64	4152	40	0.01	0.625	GO:0072401	signal transduction involved in DNA integrity checkpoint	8	DNA damage checkpoint	
1.77E-08	64	4152	40	0.01	0.625	GO:0072422	signal transduction involved in DNA damage checkpoint	9	DNA damage checkpoint	
1.40E-07	62	4152	38	0.009	0.613	GO:1902403	signal transduction involved in mitotic DNA integrity checkpoint	9	DNA damage checkpoint	
1.40E-07	62	4152	38	0.009	0.613	GO:1902402	signal transduction involved in mitotic DNA damage checkpoint	10	DNA damage checkpoint	
1.94E-07	60	4152	37	0.009	0.617	GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	12	DNA damage checkpoint	
3.04E-03	27	4152	18	0.004	0.667	GO:0043516	regulation of DNA damage response, signal transduction by p53 class mediator	8	DNA damage checkpoint	
3.60E-02	14	4152	11	0.003	0.786	GO:0006978	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	1	DNA damage checkpoint	
1.91E-10	70	4152	45	0.011	0.643	GO:0044783	G1 DNA damage checkpoint	7	DNA damage checkpoint	**DNA damage checkpoint G1** 45 unique proteins
5.55E-10	69	4152	44	0.011	0.638	GO:0031571	mitotic G1 DNA damage checkpoint	10	DNA damage checkpoint	
6.90E-08	61	4152	38	0.009	0.623	GO:1902400	intracellular signal transduction involved in G1 DNA damage checkpoint	10	DNA damage checkpoint	
6.90E-08	61	4152	38	0.009	0.623	GO:0072431	signal transduction involved in mitotic G1 DNA damage checkpoint	11	DNA damage checkpoint	
5.34E-37	274	4152	163	0.039	0.595	GO:0097193	intrinsic apoptotic signaling pathway	6	cell death - intrinsic apoptosis	**cell death via intrinsic apoptosis** 163 unique proteins
1.33E-16	149	4152	85	0.02	0.57	GO:2001242	regulation of intrinsic apoptotic signaling pathway	7	cell death - intrinsic apoptosis	
4.97E-08	73	4152	43	0.01	0.589	GO:0072332	intrinsic apoptotic signaling pathway by p53 class mediator	7	cell death - intrinsic apoptosis	
1.09E-07	52	4152	34	0.008	0.654	GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	7	cell death - intrinsic apoptosis	
1.22E-07	93	4152	50	0.012	0.538	GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	6	cell death - intrinsic apoptosis	
4.87E-67	567	4152	319	0.077	0.563	GO:0097190	apoptotic signaling pathway	5	cell death - signaling	**apoptotic signaling** 319 unique proteins
2.62E-42	368	4152	207	0.05	0.562	GO:2001233	regulation of apoptotic signaling pathway	6	cell death - signaling	
5.84E-27	171	4152	108	0.026	0.632	GO:2001235	positive regulation of apoptotic signaling pathway	6	cell death - signaling	
3.74E-18	204	4152	108	0.026	0.529	GO:2001234	negative regulation of apoptotic signaling pathway	5	cell death - signaling	
3.93E-03	9	4152	9	0.002	1	GO:0071550	death-inducing signaling complex assembly	7	cell death - signaling	
7.50E-14	103	4152	63	0.015	0.612	GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	7	DNA - damage cell death	**intrinsic apoptosis after DNA damage** 63 unique proteins
1.98E-05	42	4152	27	0.007	0.643	GO:0042771	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	8	DNA - damage cell death	
2.54E-03	34	4152	21	0.005	0.618	GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	8	DNA - damage cell death	
2.84E-59	764	4152	377	0.091	0.493	GO:0006974	cellular response to DNA damage stimulus	5	DNA - damage	**DNA damage response** 377 unique proteins
3.03E-21	119	4152	79	0.019	0.664	GO:0042770	signal transduction in response to DNA damage	6	DNA - damage	
5.68E-17	145	4152	84	0.02	0.579	GO:2001020	regulation of response to DNA damage stimulus	5	DNA - damage	
1.77E-08	64	4152	40	0.01	0.625	GO:2001022	positive regulation of response to DNA damage stimulus	5	DNA - damage	
1.28E-03	51	4152	28	0.007	0.549	GO:2001021	negative regulation of response to DNA damage stimulus	4	DNA - damage	
9.47E-03	36	4152	21	0.005	0.583	GO:0042769	DNA damage response, detection of DNA damage	6	DNA - damage	
6.88E-28	497	4152	227	0.055	0.457	GO:0006281	DNA repair	6	DNA - repair	**DNA damage repair** 227 unique proteins
1.43E-14	113	4152	68	0.016	0.602	GO:0006289	nucleotide-excision repair	7	DNA - repair	
7.49E-12	73	4152	48	0.012	0.658	GO:0006283	transcription-coupled nucleotide-excision repair	8	DNA - repair	
9.29E-08	74	4152	43	0.01	0.581	GO:0006282	regulation of DNA repair	7	DNA - repair	
3.40E-07	29	4152	23	0.006	0.793	GO:0006294	nucleotide-excision repair, preincision complex assembly	8	DNA - repair	
4.55E-06	192	4152	80	0.019	0.417	GO:0006302	double-strand break repair	7	DNA - repair	
9.79E-06	32	4152	23	0.006	0.719	GO:0070911	global genome nucleotide-excision repair	8	DNA - repair	
5.62E-05	23	4152	18	0.004	0.783	GO:0000715	nucleotide-excision repair, DNA damage recognition	6	DNA - repair	
5.69E-05	21	4152	17	0.004	0.81	GO:0006295	nucleotide-excision repair, DNA incision, 3'-to lesion	9	DNA - repair	
5.88E-05	21	4152	17	0.004	0.81	GO:0006293	nucleotide-excision repair, preincision complex stabilization	7	DNA - repair	
6.45E-04	37	4152	23	0.006	0.622	GO:0045739	positive regulation of DNA repair	8	DNA - repair	
1.99E-03	22	4152	16	0.004	0.727	GO:0000717	nucleotide-excision repair, DNA duplex unwinding	9	DNA - repair	
3.52E-03	37	4152	22	0.005	0.595	GO:0006296	nucleotide-excision repair, DNA incision, 5'-to lesion	9	DNA - repair	
3.63E-03	53	4152	28	0.007	0.528	GO:0006301	postreplication repair	7	DNA - repair	
3.70E-03	73	4152	35	0.008	0.479	GO:0000731	DNA synthesis involved in DNA repair	7	DNA - repair	
8.04E-03	72	4152	34	0.008	0.472	GO:0000726	non-recombinational repair	7	DNA - repair	
1.19E-02	39	4152	22	0.005	0.564	GO:0033683	nucleotide-excision repair, DNA incision	8	DNA - repair	
1.69E-02	65	4152	31	0.007	0.477	GO:0006303	double-strand break repair via nonhomologous end joining	8	DNA - repair	
1.01E-24	423	4152	196	0.047	0.463	GO:0009314	response to radiation	4	response to stimulus - radiation	**response to ionizing radiation** 196 unique proteins
1.82E-16	124	4152	75	0.018	0.605	GO:0009411	response to UV	6	response to stimulus - radiation	
1.20E-14	141	4152	79	0.019	0.56	GO:0010212	response to ionizing radiation	5	response to stimulus - radiation	
2.57E-08	158	4152	74	0.018	0.468	GO:0071478	cellular response to radiation	5	response to stimulus - radiation	
5.33E-07	64	4152	38	0.009	0.594	GO:0034644	cellular response to UV	7	response to stimulus - radiation	
2.08E-06	56	4152	34	0.008	0.607	GO:0071479	cellular response to ionizing radiation	6	response to stimulus - radiation	
3.61E-06	50	4152	31	0.007	0.62	GO:0010332	response to gamma radiation	6	response to stimulus - radiation	
7.99E-05	32	4152	22	0.005	0.688	GO:0010165	response to X-ray	6	response to stimulus - radiation	
5.03E-19	211	4152	112	0.027	0.531	GO:0034599	cellular response to oxidative stress	5	stress - oxidative	**response to oxidative stress** 167 unique proteins
9.61E-19	373	4152	167	0.04	0.448	GO:0006979	response to oxidative stress	4	stress - oxidative	
3.54E-16	120	4152	73	0.018	0.608	GO:0042542	response to hydrogen peroxide	6	stress - oxidative	
1.89E-15	203	4152	103	0.025	0.507	GO:0000302	response to reactive oxygen species	5	stress - oxidative	
6.27E-12	123	4152	68	0.016	0.553	GO:0034614	cellular response to reactive oxygen species	6	stress - oxidative	
1.05E-10	74	4152	47	0.011	0.635	GO:0070301	cellular response to hydrogen peroxide	7	stress - oxidative	
1.02E-09	58	4152	39	0.009	0.672	GO:1900407	regulation of cellular response to oxidative stress	5	stress - oxidative	
8.48E-09	63	4152	40	0.01	0.635	GO:1902882	regulation of response to oxidative stress	5	stress - oxidative	
7.99E-05	32	4152	22	0.005	0.688	GO:1902883	negative regulation of response to oxidative stress	4	stress - oxidative	
7.99E-05	32	4152	22	0.005	0.688	GO:1900408	negative regulation of cellular response to oxidative stress	4	stress - oxidative	
7.99E-05	32	4152	22	0.005	0.688	GO:1901031	regulation of response to reactive oxygen species	6	stress - oxidative	
3.18E-02	16	4152	12	0.003	0.75	GO:1900409	positive regulation of cellular response to oxidative stress	5	stress - oxidative	
2.20E-31	256	4152	148	0.036	0.578	GO:0034976	response to endoplasmic reticulum stress	5	ER - stress	**ER stress** 148 unique proteins
5.04E-06	38	4152	26	0.006	0.684	GO:1903573	negative regulation of response to endoplasmic reticulum stress	4	ER - stress	
1.45E-20	83	4152	62	0.015	0.747	GO:0036503	ERAD pathway	1	ubiquitin-proteasome - ER	**ER ubiquitin-proteasome** 113 unique proteins
1.28E-15	66	4152	49	0.012	0.742	GO:0030433	ER-associated ubiquitin-dependent protein catabolic process	2	ubiquitin-proteasome - ER	
3.14E-09	127	4152	65	0.016	0.512	GO:0030968	endoplasmic reticulum unfolded protein response	5	ubiquitin-proteasome - ER	
3.30E-07	27	4152	22	0.005	0.815	GO:1904292	regulation of ERAD pathway	2	ubiquitin-proteasome - ER	
3.93E-03	9	4152	9	0.002	1	GO:1903069	regulation of ER-associated ubiquitin-dependent protein catabolic process	3	ubiquitin-proteasome - ER	
9.69E-03	13	4152	11	0.003	0.846	GO:1904294	positive regulation of ERAD pathway	2	ubiquitin-proteasome - ER	
3.68E-02	12	4152	10	0.002	0.833	GO:1904293	negative regulation of ERAD pathway	2	ubiquitin-proteasome - ER	
3.77E-18	177	4152	98	0.024	0.554	GO:0035966	response to topologically incorrect protein	4	UPR	**UPR** 98 unique proteins
7.62E-15	167	4152	89	0.021	0.533	GO:0006986	response to unfolded protein	5	UPR	
8.22E-13	138	4152	75	0.018	0.543	GO:0035967	cellular response to topologically incorrect protein	5	UPR	
9.24E-10	130	4152	67	0.016	0.515	GO:0034620	cellular response to unfolded protein	6	UPR	
6.48E-04	15	4152	13	0.003	0.867	GO:0051788	response to misfolded protein	5	UPR	
1.87E-03	12	4152	11	0.003	0.917	GO:0071218	cellular response to misfolded protein	6	UPR	
8.95E-08	28	4152	23	0.006	0.821	GO:1903513	endoplasmic reticulum to cytosol transport	5	ER - transport	**ER transport** 25 unique proteins
8.95E-08	28	4152	23	0.006	0.821	GO:0030970	retrograde protein transport, ER to cytosol	2	ER - transport	
6.40E-08	36	4152	25	0.006	0.694	GO:0032527	protein exit from endoplasmic reticulum	6	ER - transport	
2.19E-38	482	4152	242	0.058	0.502	GO:0072657	protein localization to membrane	6	protein localization - membrane	**protein localization to membranes** 242 unique proteins
1.16E-34	357	4152	191	0.046	0.535	GO:0090150	establishment of protein localization to membrane	7	protein localization - membrane	
2.04E-25	94	4152	72	0.017	0.766	GO:0006614	SRP-dependent cotranslational protein targeting to membrane	9	protein localization - membrane	
1.38E-23	102	4152	74	0.018	0.725	GO:0006613	cotranslational protein targeting to membrane	8	protein localization - membrane	
1.70E-20	186	4152	105	0.025	0.565	GO:0006612	protein targeting to membrane	7	protein localization - membrane	
2.22E-07	201	4152	86	0.021	0.428	GO:0072659	protein localization to plasma membrane	6	protein localization - membrane	
7.99E-05	32	4152	22	0.005	0.688	GO:0051204	protein insertion into mitochondrial membrane	7	protein localization - membrane	
1.49E-04	137	4152	59	0.014	0.431	GO:0090002	establishment of protein localization to plasma membrane	7	protein localization - membrane	
3.18E-04	46	4152	27	0.007	0.587	GO:0051205	protein insertion into membrane	6	protein localization - membrane	
7.36E-03	63	4152	31	0.007	0.492	GO:1903076	regulation of protein localization to plasma membrane	6	protein localization - membrane	
4.72E-41	344	4152	196	0.047	0.57	GO:0034504	protein localization to nucleus	7	protein localization -nucleus	**protein localization to nucleus** 235 unique proteins
2.28E-30	209	4152	128	0.031	0.612	GO:1900180	regulation of protein localization to nucleus	6	protein localization -nucleus	
1.31E-27	263	4152	145	0.035	0.551	GO:0044744	protein targeting to nucleus	7	protein localization -nucleus	
1.31E-27	263	4152	145	0.035	0.551	GO:0006606	protein import into nucleus	6	protein localization -nucleus	
1.28E-18	121	4152	74	0.018	0.612	GO:1900182	positive regulation of protein localization to nucleus	5	protein localization -nucleus	
8.55E-10	72	4152	45	0.011	0.625	GO:1900181	negative regulation of protein localization to nucleus	4	protein localization -nucleus	
2.42E-04	56	4152	31	0.007	0.554	GO:0006611	protein export from nucleus	6	protein localization -nucleus	
1.26E-03	26	4152	18	0.004	0.692	GO:0070198	protein localization to chromosome, telomeric region	8	protein localization - nucleus	
1.89E-03	60	4152	31	0.007	0.517	GO:0034502	protein localization to chromosome	7	protein localization - nucleus	
7.70E-03	11	4152	10	0.002	0.909	GO:1904816	positive regulation of protein localization to chromosome, telomeric region	5	protein localization -nucleus	
1.76E-02	8	4152	8	0.002	1	GO:1904869	regulation of protein localization to Cajal body	7	protein localization - nucleus	
1.76E-02	8	4152	8	0.002	1	GO:1904871	positive regulation of protein localization to Cajal body	6	protein localization - nucleus	
3.14E-02	10	4152	9	0.002	0.9	GO:0070203	regulation of establishment of protein localization to telomere	1	protein localization - nucleus	
1.55E-141	5195	4152	1837	0.442	0.354	GO:0010467	gene expression	5	gene expression	**gene expression** 1837 unique proteins
4.34E-106	4201	4152	1489	0.359	0.354	GO:0010468	regulation of gene expression	5	gene expression	
5.47E-81	1616	4152	696	0.168	0.431	GO:0010628	positive regulation of gene expression	6	gene expression	
9.03E-71	1416	4152	612	0.147	0.432	GO:0010629	negative regulation of gene expression	5	gene expression	
1.42E-53	453	4152	256	0.062	0.565	GO:0010608	posttranscriptional regulation of gene expression	6	gene expression	
1.77E-18	250	4152	125	0.03	0.5	GO:0040029	regulation of gene expression, epigenetic	6	gene expression	
2.08E-08	56	4152	34	0.008	0.607	GO:0032922	circadian regulation of gene expression	6	gene expression	
1.13E-67	3667	4152	1239	0.298	0.338	GO:0097659	nucleic acid-templated transcription	8	transcription	**transcription** 1296 unique proteins
2.39E-66	3656	4152	1232	0.297	0.337	GO:0006351	transcription, DNA-templated	9	transcription	
5.43E-62	3503	4152	1178	0.284	0.336	GO:1903506	regulation of nucleic acid-templated transcription	8	transcription	
2.86E-60	3486	4152	1168	0.281	0.335	GO:0006355	regulation of transcription, DNA-templated	9	transcription	
1.93E-56	1286	4152	540	0.13	0.42	GO:1903508	positive regulation of nucleic acid-templated transcription	8	transcription	
1.93E-56	1286	4152	540	0.13	0.42	GO:0045893	positive regulation of transcription, DNA-templated	9	transcription	
4.41E-43	1121	4152	458	0.11	0.409	GO:1903507	negative regulation of nucleic acid-templated transcription	8	transcription	
5.83E-42	1084	4152	444	0.107	0.41	GO:0045892	negative regulation of transcription, DNA-templated	9	transcription	
5.64E-11	119	4152	65	0.016	0.546	GO:0006354	DNA-templated transcription, elongation	8	transcription	
1.98E-04	22	4152	17	0.004	0.773	GO:0000470	maturation of LSU-rRNA	6	transcription	
1.95E-02	27	4152	17	0.004	0.63	GO:0009303	rRNA transcription	1	transcription	
4.49E-65	1956	4152	761	0.183	0.389	GO:0006366	transcription from RNA polymerase II promoter	10	transcription - pol II promoter	**transcription - RNA pol II** 761 unique proteins
3.45E-57	1761	4152	684	0.165	0.388	GO:0006357	regulation of transcription from RNA polymerase II promoter	10	transcription - pol II promoter	
2.17E-41	981	4152	411	0.099	0.419	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	10	transcription - pol II promoter	
1.25E-38	719	4152	322	0.078	0.448	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	10	transcription - pol II promoter	
3.85E-14	173	4152	90	0.022	0.52	GO:0006367	transcription initiation from RNA polymerase II promoter	9	transcription - pol II promoter	
3.50E-11	61	4152	42	0.01	0.689	GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	11	transcription - pol II promoter	
1.67E-08	92	4152	51	0.012	0.554	GO:0006368	transcription elongation from RNA polymerase II promoter	9	transcription - pol II promoter	
9.79E-06	32	4152	23	0.006	0.719	GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	12	transcription - pol II promoter	
1.52E-04	26	4152	19	0.005	0.731	GO:1901522	positive regulation of transcription from RNA polymerase II pro	11	transcription - pol II promoter	
7.96E-04	61	4152	32	0.008	0.525	GO:0006369	termination of RNA polymerase II transcription	9	transcription - pol II promoter	
1.62E-02	22	4152	15	0.004	0.682	GO:0036003	positive regulation of transcription from RNA polymerase II promoter in response to stress	11	transcription - pol II promoter	
3.70E-02	23	4152	15	0.004	0.652	GO:0060260	regulation of transcription initiation from RNA polymerase II promoter	11	transcription - pol II promoter	
6.81E-45	645	4152	310	0.075	0.481	GO:0006412	translation	6	translation	**translation** 394 unique proteins
6.07E-39	189	4152	130	0.031	0.688	GO:0006413	translational initiation	4	translation	
3.99E-35	328	4152	181	0.044	0.552	GO:0006417	regulation of translation	6	translation	
7.41E-33	308	4152	170	0.041	0.552	GO:0042254	ribosome biogenesis	5	translation	
2.40E-17	136	4152	81	0.02	0.596	GO:0017148	negative regulation of translation	6	translation	
2.28E-11	94	4152	56	0.013	0.596	GO:0045727	positive regulation of translation	7	translation	
4.67E-10	81	4152	49	0.012	0.605	GO:0006446	regulation of translational initiation	7	translation	
2.68E-07	58	4152	36	0.009	0.621	GO:0042273	ribosomal large subunit biogenesis	5	translation	
6.92E-07	52	4152	33	0.008	0.635	GO:0002181	cytoplasmic translation	7	translation	
2.02E-06	61	4152	36	0.009	0.59	GO:0042274	ribosomal small subunit biogenesis	5	translation	
7.62E-05	54	4152	31	0.007	0.574	GO:0042255	ribosome assembly	6	translation	
1.62E-02	22	4152	15	0.004	0.682	GO:0045947	negative regulation of translational initiation	7	translation	
3.70E-02	23	4152	15	0.004	0.652	GO:0000027	ribosomal large subunit assembly	7	translation	

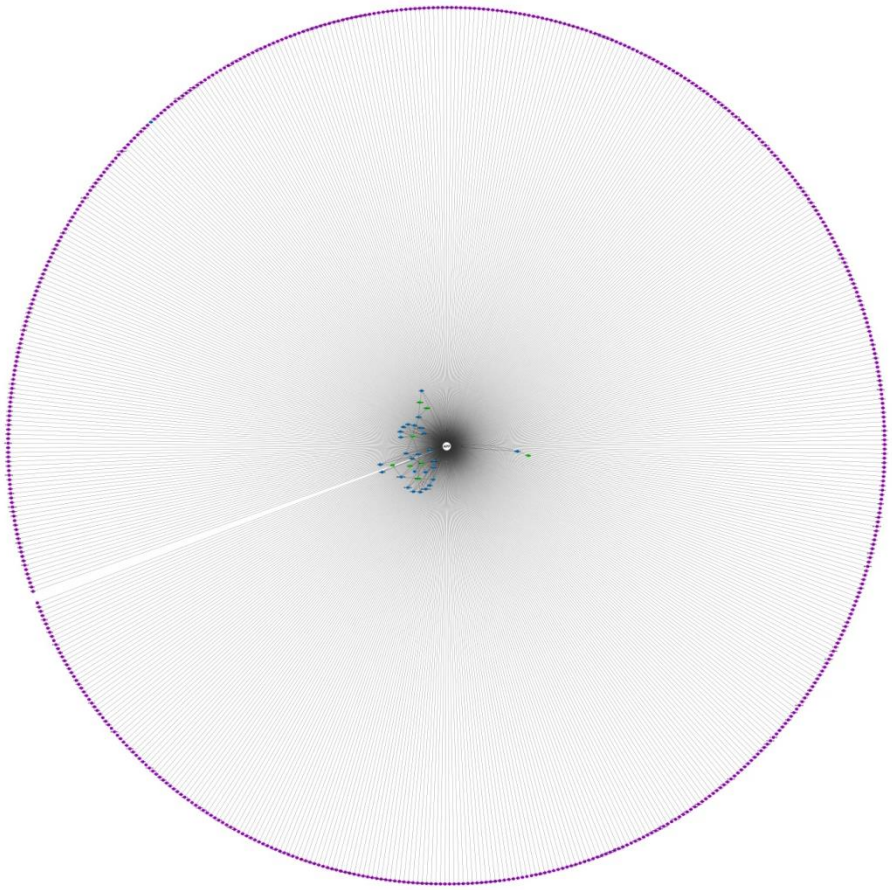
Supporting Table 7

DNA-DAMAGE CONTROL (BLACK)	GENE EXPRESSION (BLACK)		GENE EXPRESSION (PURPLE)		WASTE (PURPLE)
Q9Y2T1	O43707	P51610	Q9Y4W6	P48556	Q9UKV5
O60885	O00468	O14964	Q12955	P61289	O43681
P24385	P32121	P48551	P05067-APP	P60484	P54252
O75909	Q99700	Q12906	O60306	Q13610	P51572
Q99741	Q9Y2T1	Q92993	Q14865	P78406	Q9NZS9
P49674	Q5H9F3	Q9Y2K7	O00327	P62826	Q96A33
Q01094	O60885	Q92945	Q6PL18	P06400	O43889
Q16254	Q9HCU9	O15525	P54252	Q16576	Q9BUN8
Q09472-EP300	O95503	P61244	Q92934	Q96PK6	Q9GZP9
P18074	P24385	P56270	Q96RK4	Q9NVW2	P31689
Q5XUX0	O75909	Q9UIS9	Q9H6U6	P62979	P25685
Q7Z6Z7	Q99741	Q96EZ8	Q96G01	O76021	P05198
Q92993	Q9HCK8	Q96RN5	Q6RI45	Q92541	Q96HE7
Q9Y2K7	Q96RK0	O75448	Q9Y297	Q96T21	P14625
Q96EZ8	Q99829	Q7Z7M0	Q07021	P28370	Q92598
O00255	Q10570	O00255	Q86VP6	P63162	Q8TAT6
P14174	Q8N684	P14174	Q14444	P18583	Q13438
Q14686	P49674	Q9HBH9	P22681	P35711	P17980
P24928	O60716	Q9HAP2	O95931	Q9UJZ1	P62195
O75807	Q8TDD1	Q99583	P78396	Q13033	Q9BV68
Q99873	P26358	Q7Z7H8	P13987	Q9Y5B9	Q96GF1
P54725	Q01094	Q9BQG0	Q9HD42	Q9BSH4	P60468
Q96PK6	Q16254	Q14686	Q969X6	Q6P1X5	Q9UBV2
Q12824	Q96KS0	Q9Y618	Q9UIV1	Q9UHD2	Q8NHG7
Q08945	Q9Y262	Q15653	P61201	Q15369	O14656
O43463	Q09472-EP300	Q9Y3T9	Q16630	Q12888	O60858
Q15554	P18074	P20393	O43889	O60858	Q96B02
P63279	Q92800	Q5SRE5	P46108	Q8WWH5	Q9UMX0
O14933	Q14254	Q8IZL8	P19784	Q99816	P54578
Q92900	Q12789	O15534	Q12996	Q9NUQ3	Q9UHP3
Q9P1Z0	O00178	O15055	Q13617	P51668	O95292
	O00541	P09012	Q9P013	Q05086	P55072-VCP
	Q99623	Q02086	Q9NQC7	P22695	P17861
	Q9BY77	Q12772	P53355	Q9Y4E8	
	P24928	Q9UQ35	O43293	Q93009	
	O75807	Q08945	O00571	Q93008	
	Q9Y478	P42226	Q9H0S4	Q9Y5J1	
	Q99873	O00267	P26196	Q9UBK9	
	O43242	O43463	P49366	Q9BRP8	
	Q92530	P20226	Q9Y295	P17861	
	Q9H7Z7	Q15554	Q9BV47	Q8IY57	
	Q86YD1	Q04726	P63167	P31946	
	P10276	Q9UPQ9	Q15029	Q86T24	
	Q96PK6	Q13114	Q9P2K8	Q8TD23	
	Q96EP0	Q92574	P41252	P49770	
	P46779	P49411	P17181	P05198	
	Q8N122	P26368	P78318	P55010	
	Q9Y467	P63279	Q9NV31	Q9BQ52	
	Q5PRF9	P68036	P48200	Q15717-ELAVL1	
	Q9H4L4	Q92900	Q15046	Q96HE7	
	Q15637	O75604	Q9Y4X4	P51116	
	Q15459	Q9UPT9	Q13601	P15170	
	Q15393	Q969T9	Q92615	Q8IYD1	
	Q96ST3	O00308	Q9Y2U8	P32780	
	Q02978	Q9P1Z0	Q8WVC0	Q9UKN8	
	Q13485	Q14202	Q02750	O94992	
	O15105	Q8TF68	P28482	P49773	
	P51532	Q96KM6	P45983	Q9NP66	
	Q12824	Q6ZN55	Q7Z7M0	Q92598	
			Q9NPJ1	Q8N1F7	
			P42568	P52948	
			Q9UH92	O15530	
			Q13084	P19387	
			Q9BQ48	P35813	
			Q13405	P36873	
			Q9BYN8	O14974	
			Q9Y2R9	P16298	
			Q9NVV4	P30048	
			O75592	P54619	
			Q09161	P10644	
			Q15596	P78527	
			Q9Y6Q9	O14744	
			Q99608	F7VJQ1	
			Q96PU5	P25788	
			Q15843	P25789	
			P21359	O14818	
			P55769	P49720	
			Q9ULX3	Q99436	
			Q14978	P17980	
			O43809	P62195	
			Q9UKX7	O00232	

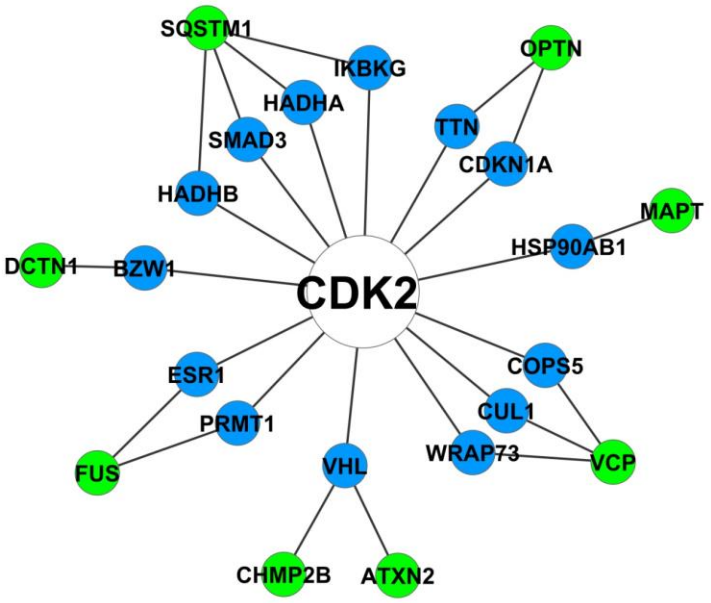
Supporting Figure S1

EntrezA	SwissA	NameA	EntrezB	SwissB	NameB	Taxid.interactor.A	Taxid.interactor.B	Method	Author	PubMed ID
8945	Q9Y297	BTRC BTRCP FBW1A FBXW1A	468	P18848	ATF4 CREB2 TXREB	taxid:9606(Human)	taxid:9606(Human)	*psi-mi:MI:0686(unspecified method)*	Pons et al.(2008)	pubmed:1805225
196	P35869	AHR BHLHE76	*mouse*	*P00184*	*mouse*	taxid:9606(Human)	*taxid:10090(Mouse)*	psi-mi:MI:0686(unspecified method)	Vasiliou et al. (1995)	*pubmed:2550446|pubmed:8849333 |pubmed:11382553|pubmed:8215422| pubmed:1312672|pubmed:7506016|pubmed:2173716*
26574	Q9NY61	AATF CHE1 DED HSPC277	*TrEMBL D6RA96*		*TrEMBL*	taxid:9606(Human)	taxid:9606(Human)	psi-mi:"MI:0007"(anti tag coimmunoprecipitation)	Hein et al.	*pubmed:unassigned1268|imex:IM-24272*

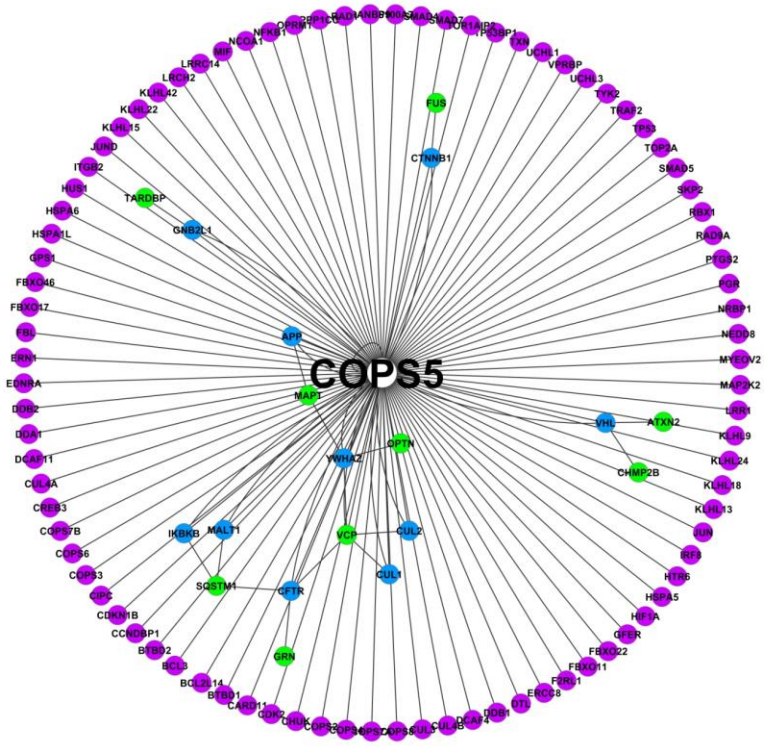
Supporting Figure S2



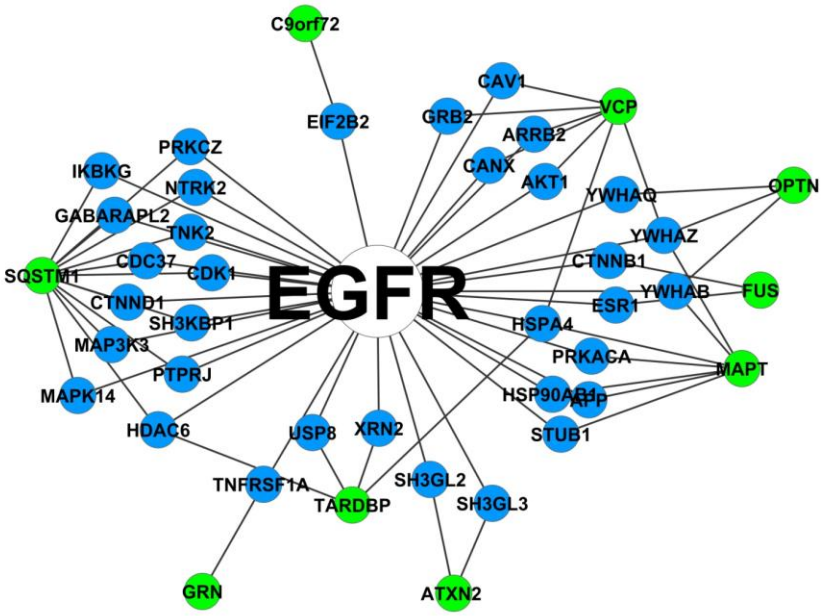
Supporting Figure S3



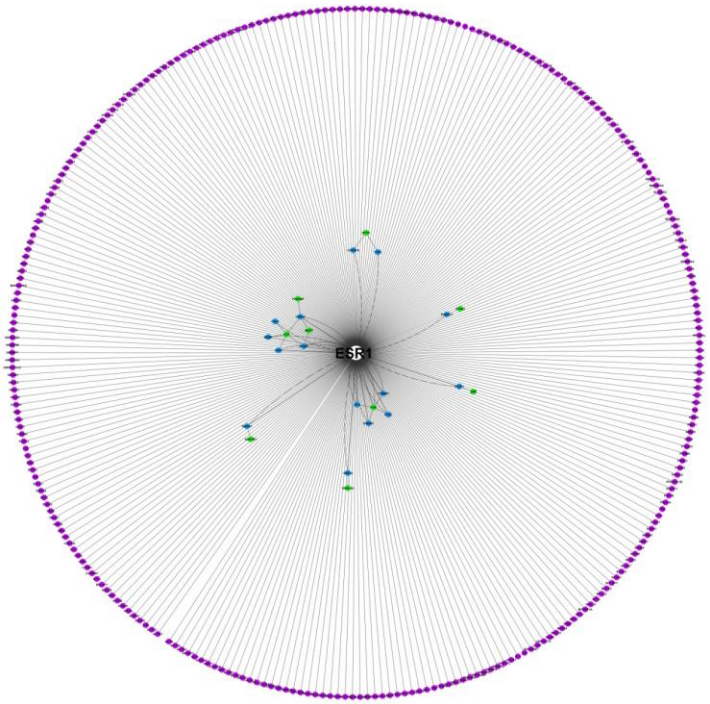
Supporting Figure S4



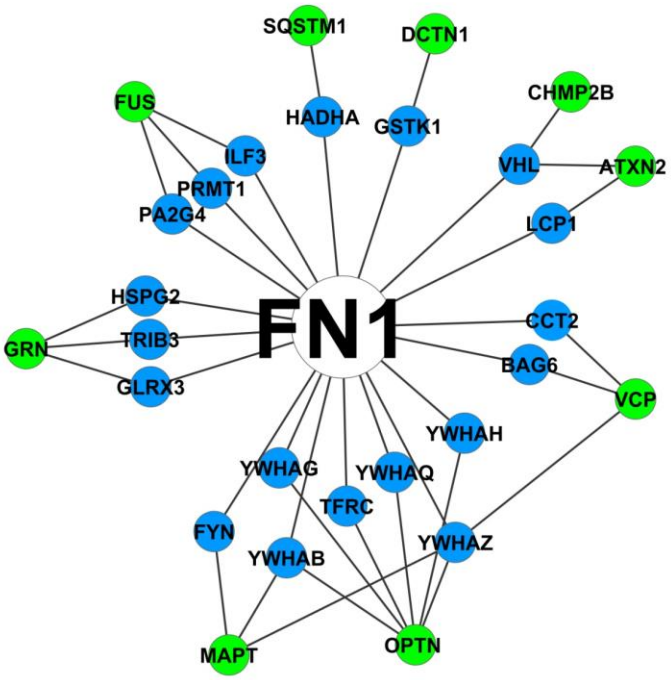
Supporting Figure S5



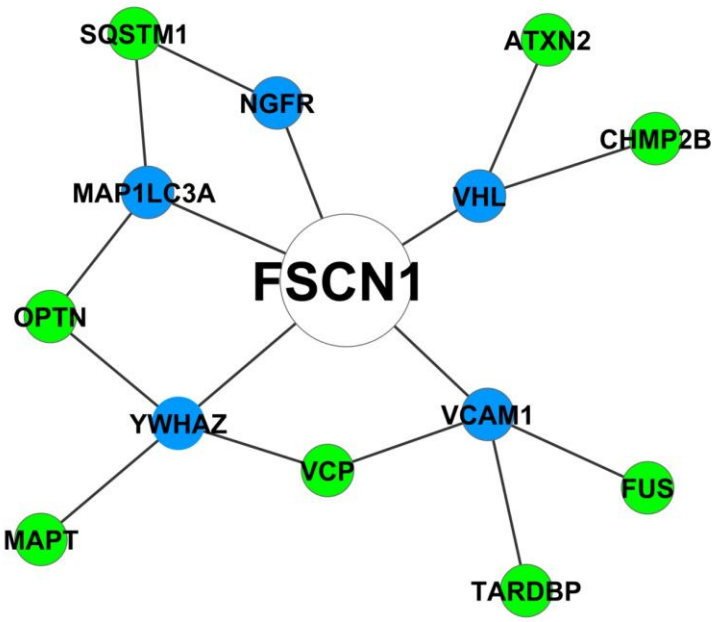
Supporting Figure S6



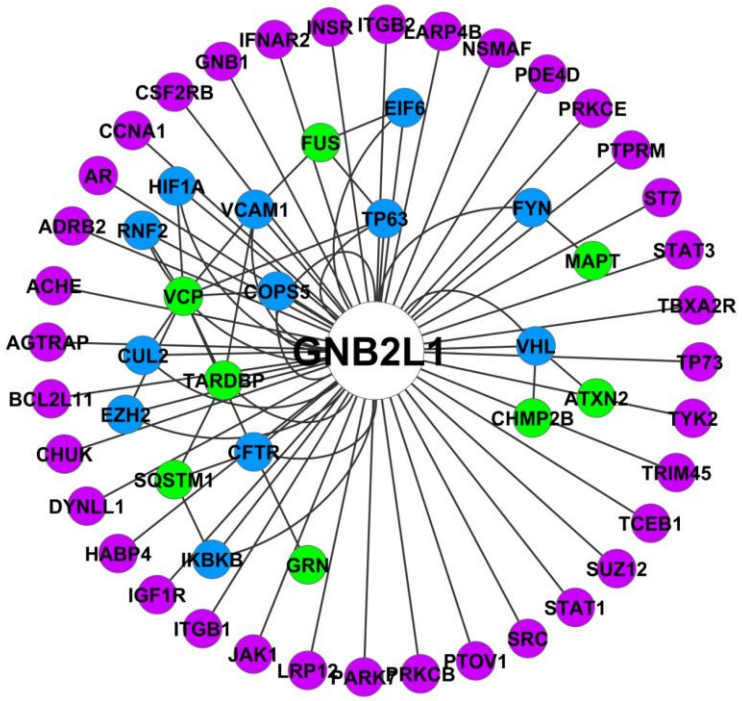
Supporting Figure S7



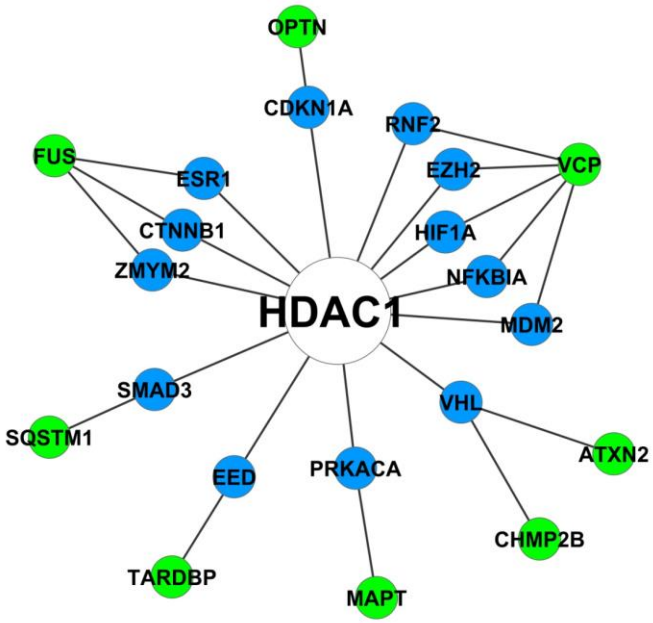
Supporting Figure S8



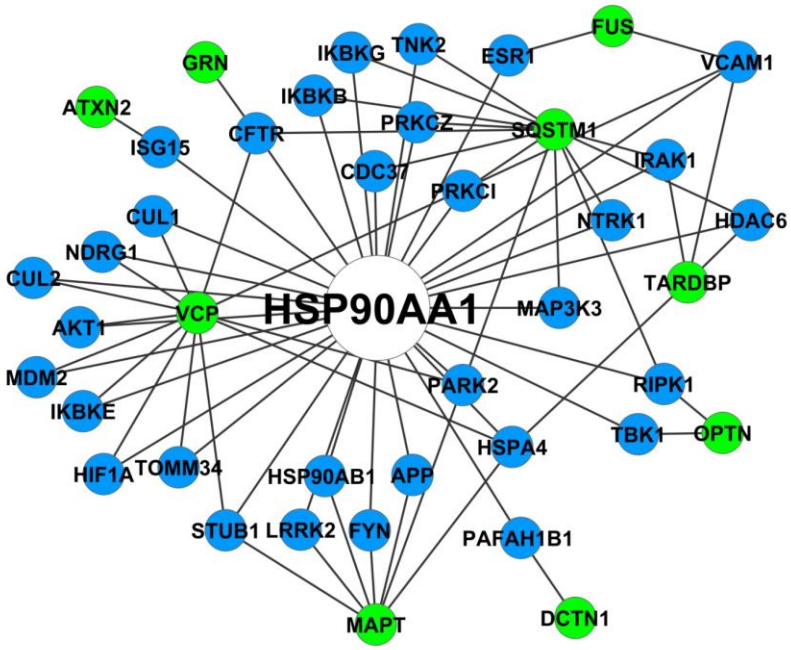
Supporting Figure S9



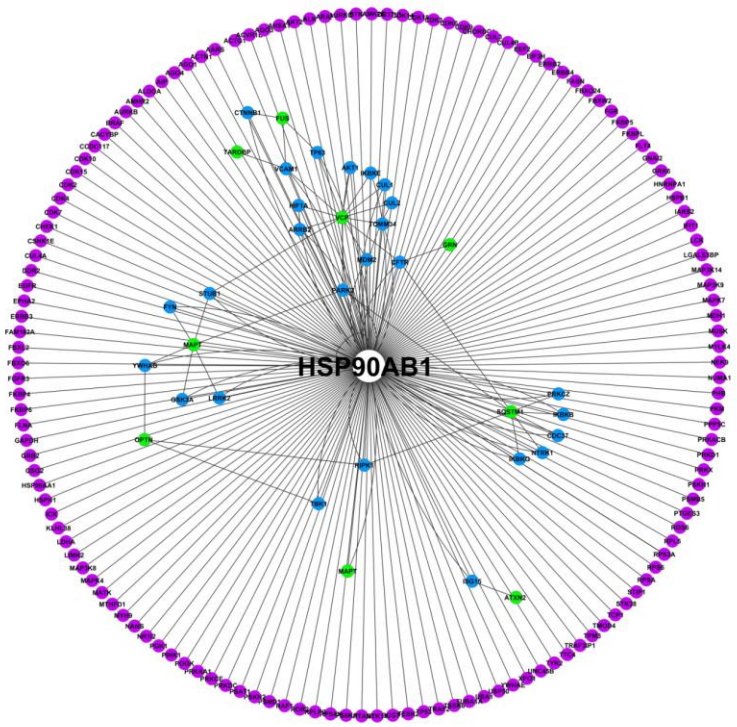
Supporting Figure S10



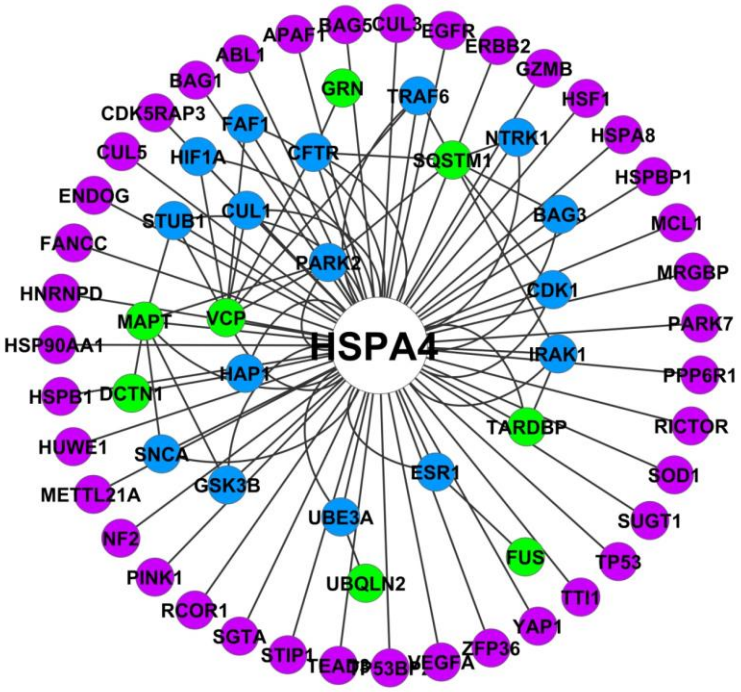
Supporting Figure S11



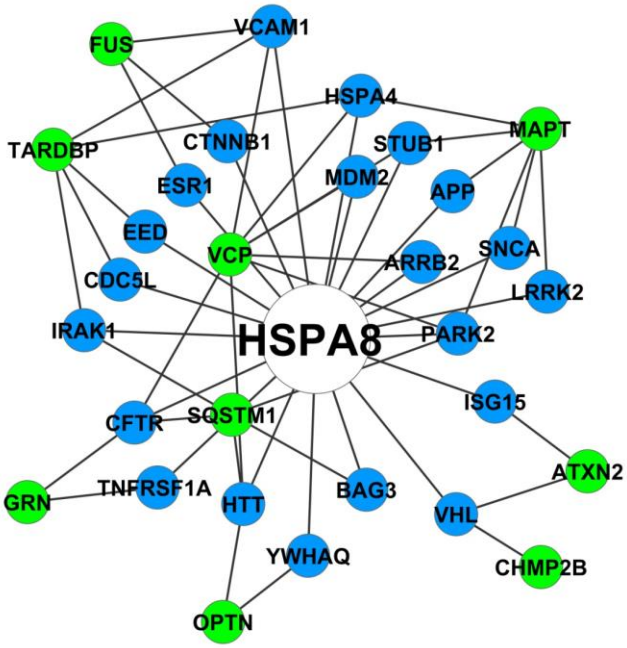
Supporting Figure S12



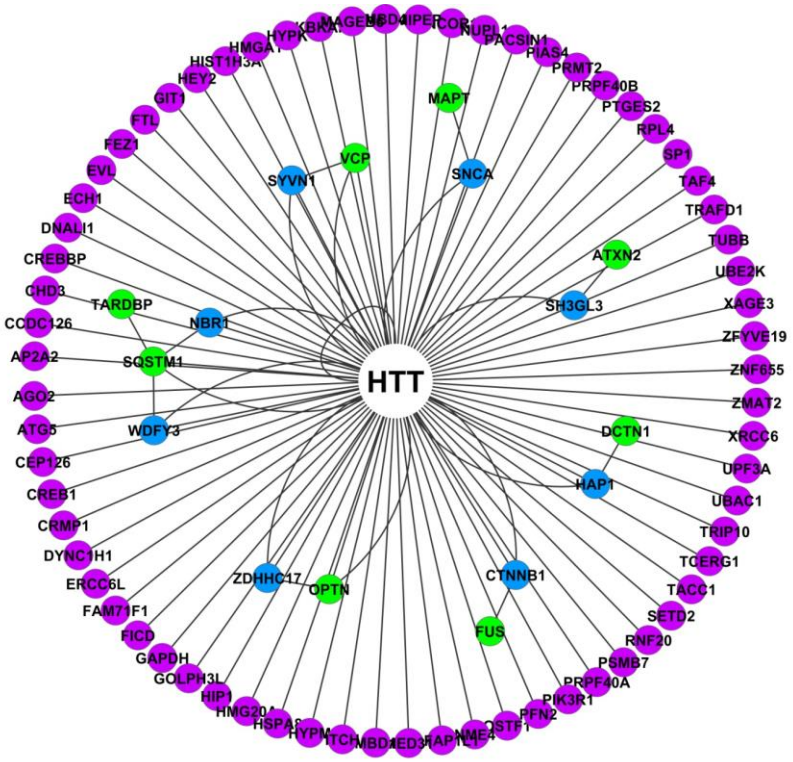
Supporting Figure S13



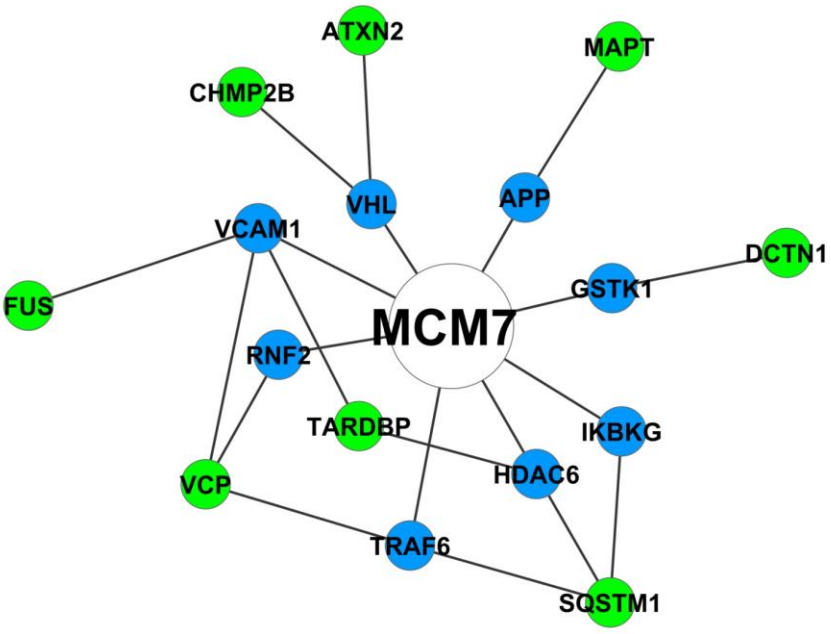
Supporting Figure S14



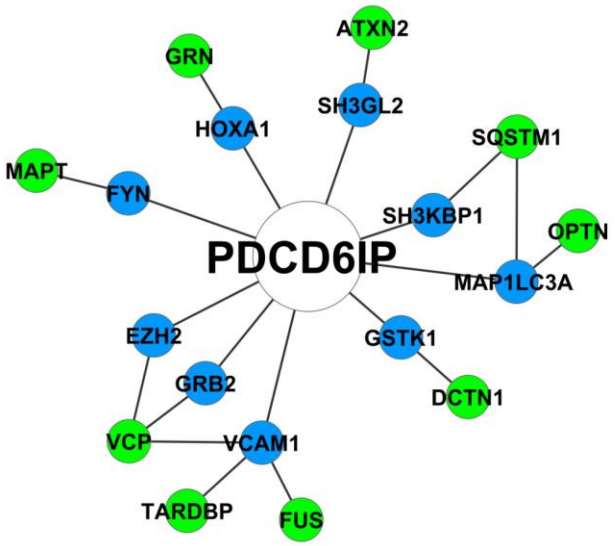
Supporting Figure S15



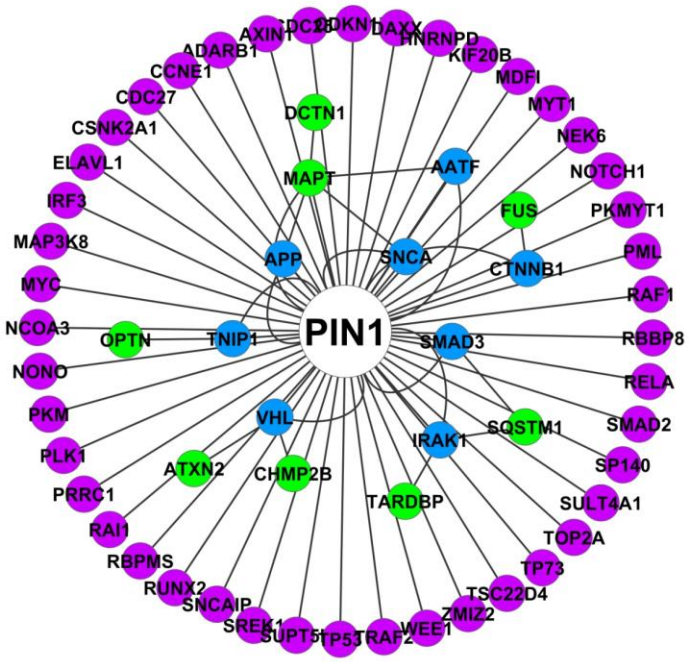
Supporting Figure S16



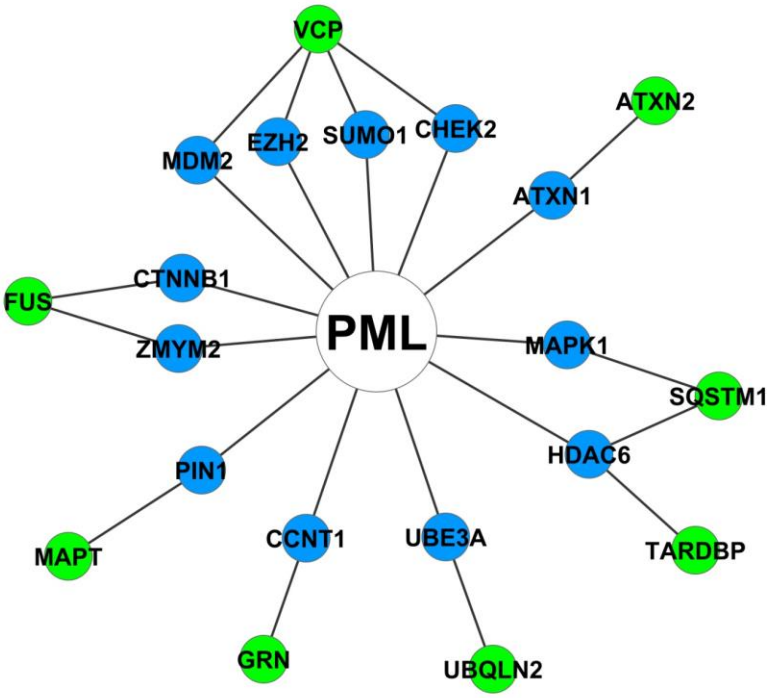
Supporting Figure S17



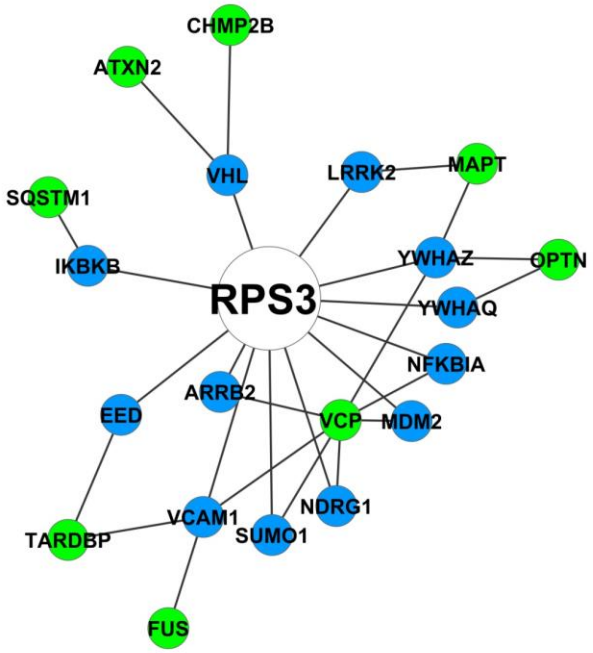
Supporting Figure S18



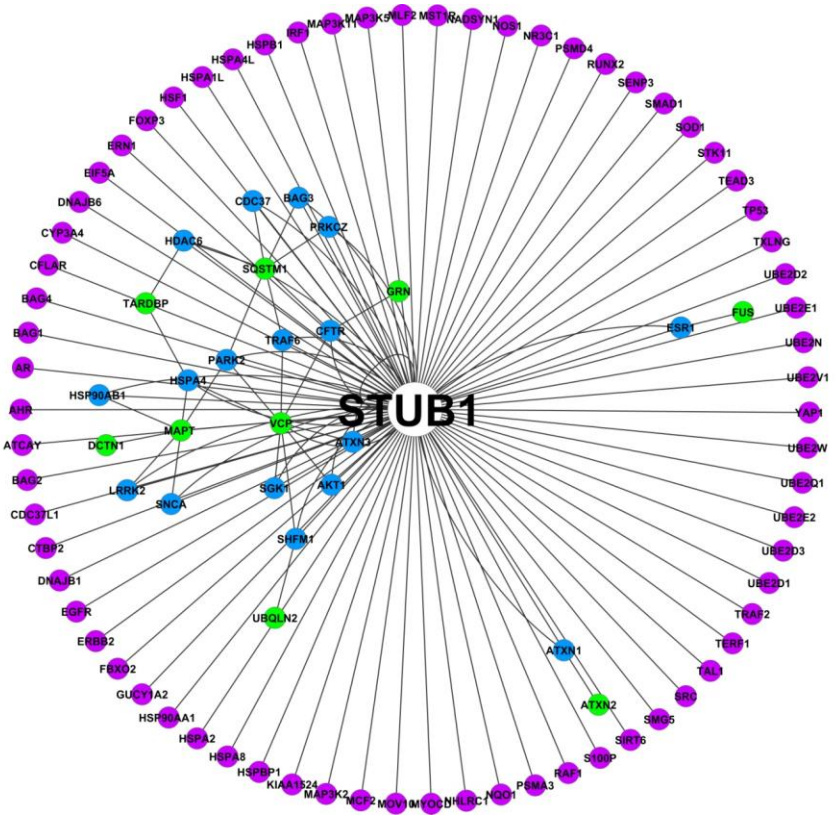
Supporting Figure S19



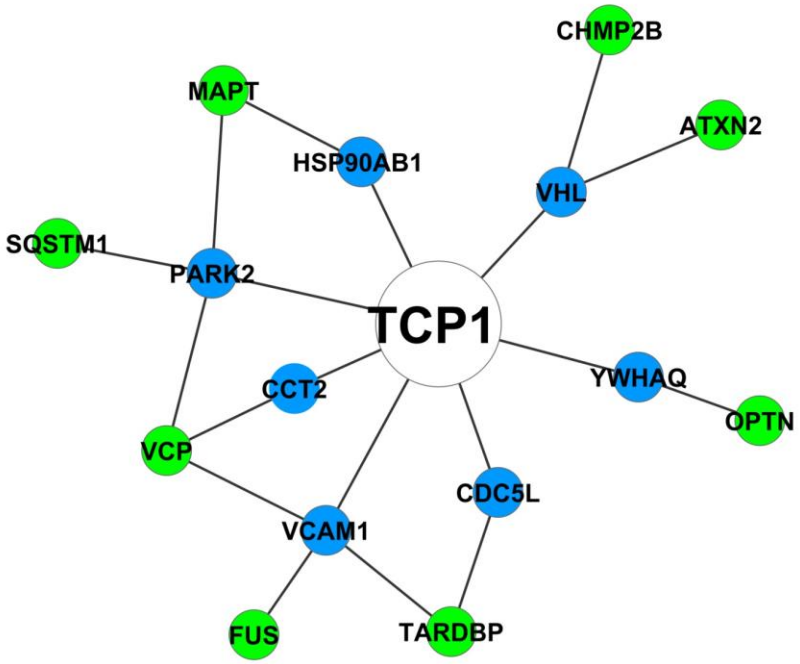
Supporting Figure S20



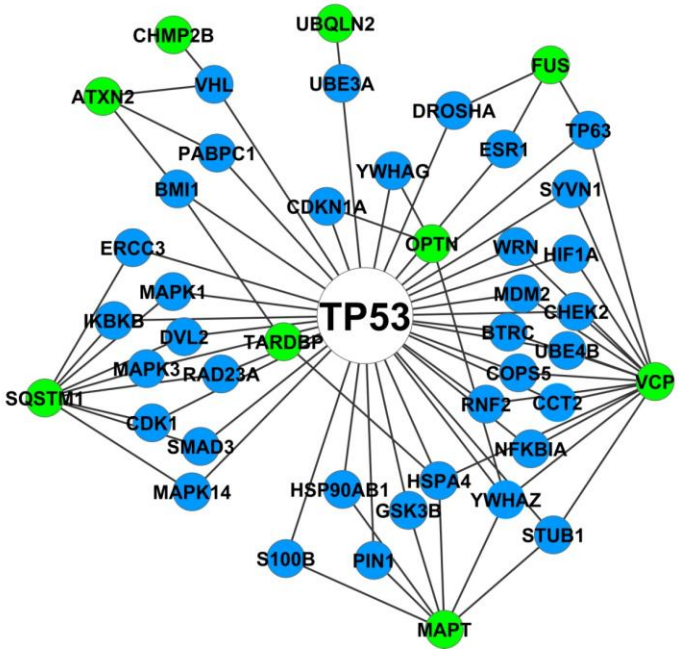
Supporting Figure S21



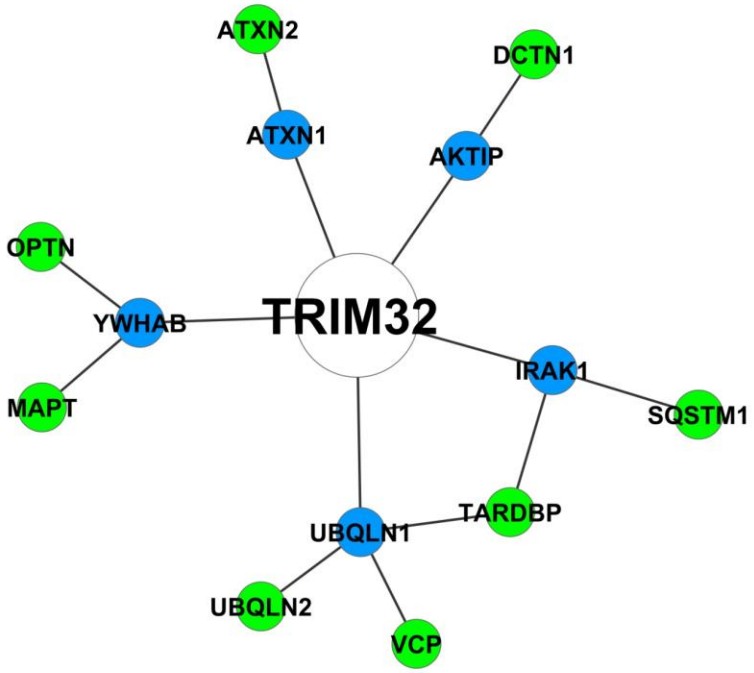
Supporting Figure S22



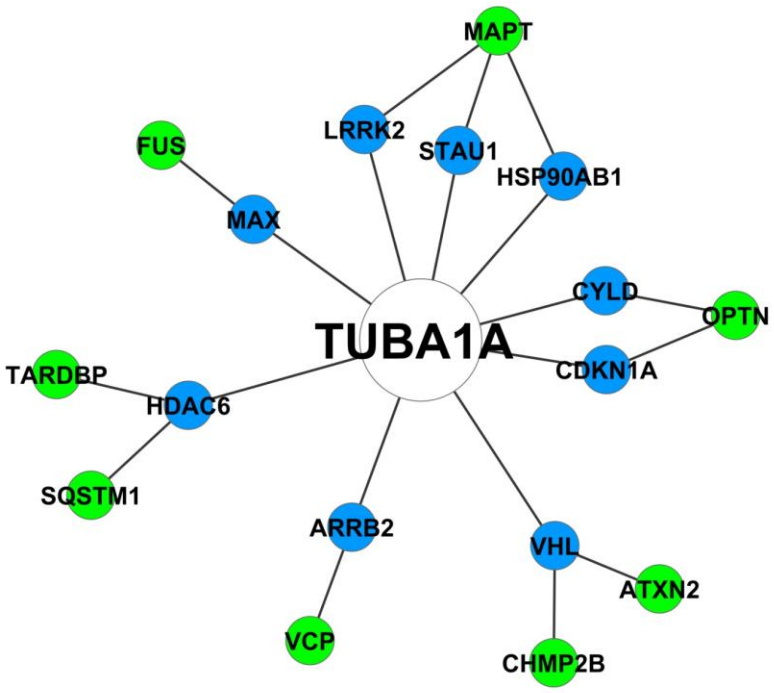
Supporting Figure S23



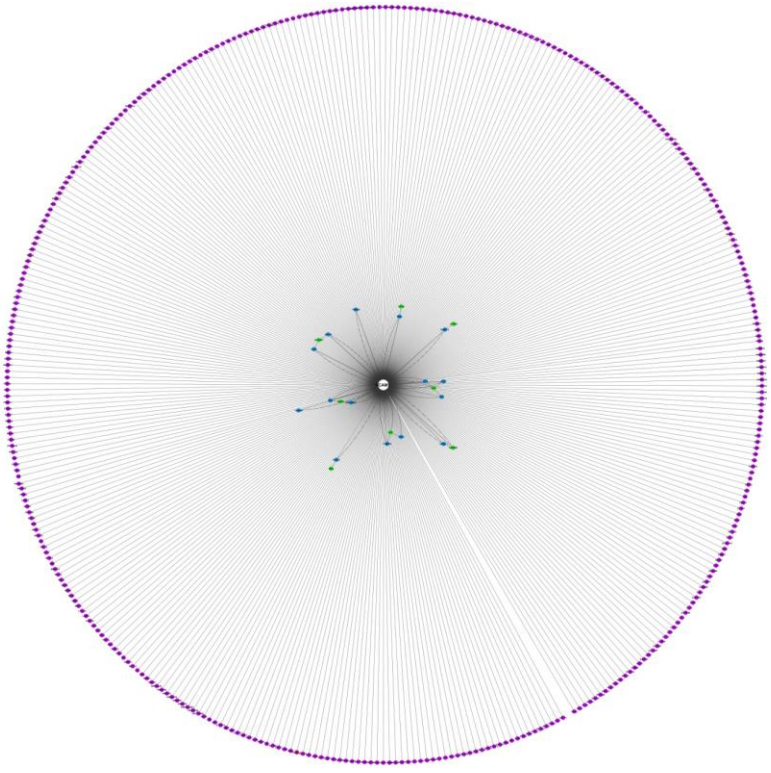
Supporting Figure S24



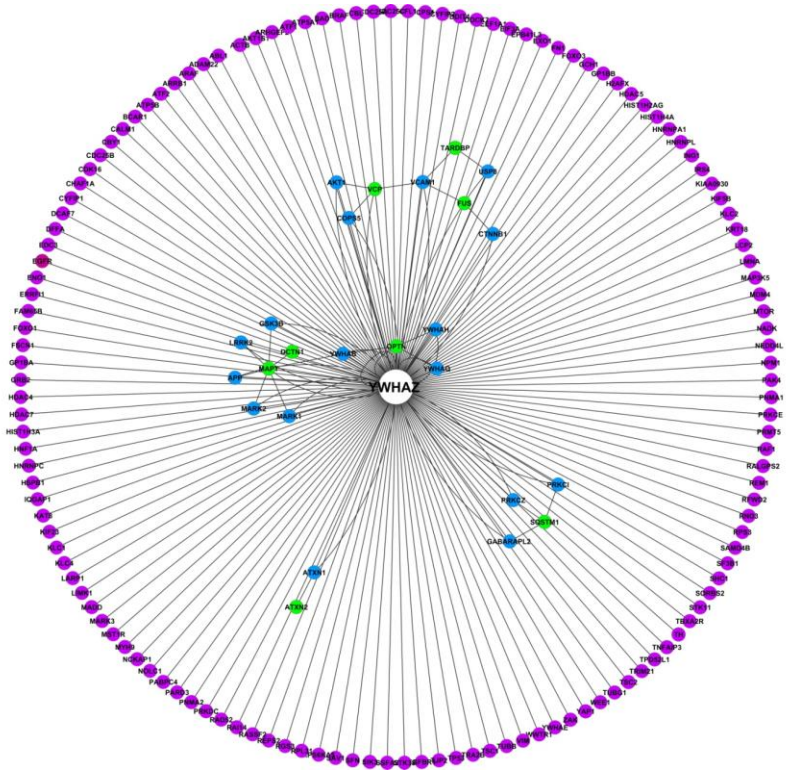
Supporting Figure S25



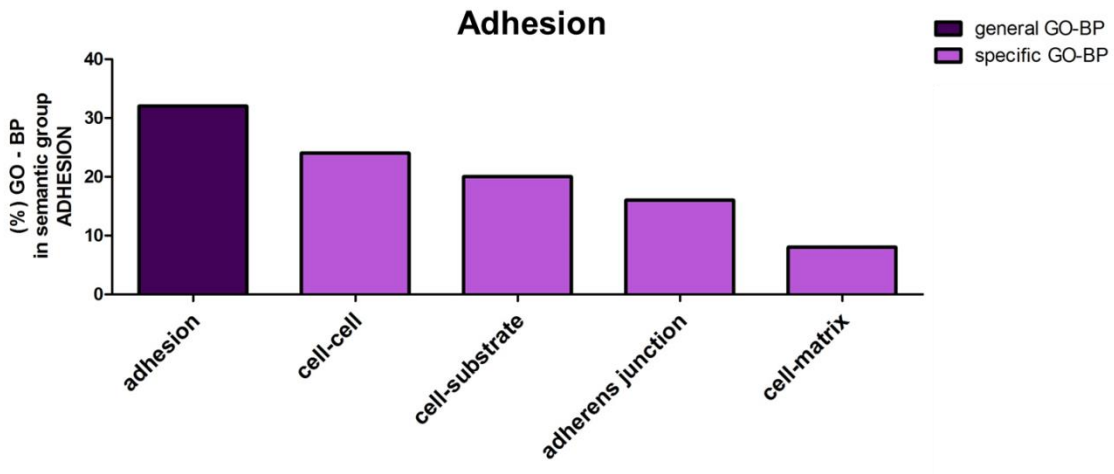
Supporting Figure S26



Supporting Figure S27

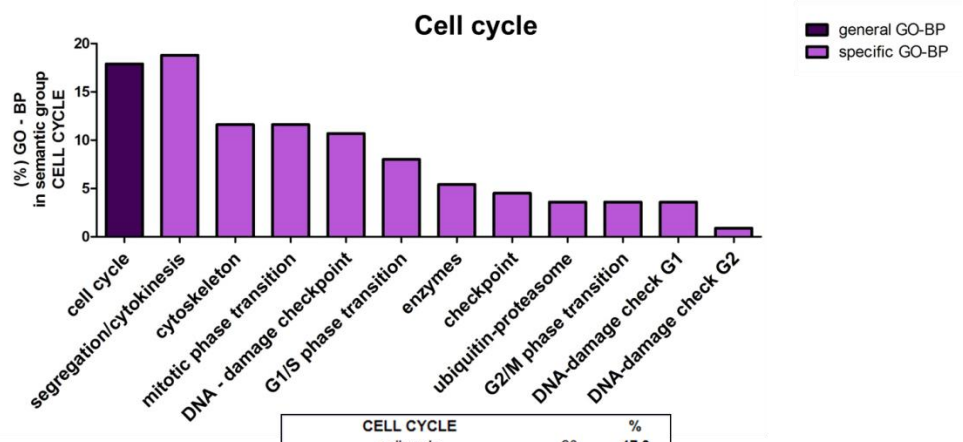


Supporting Figure S28



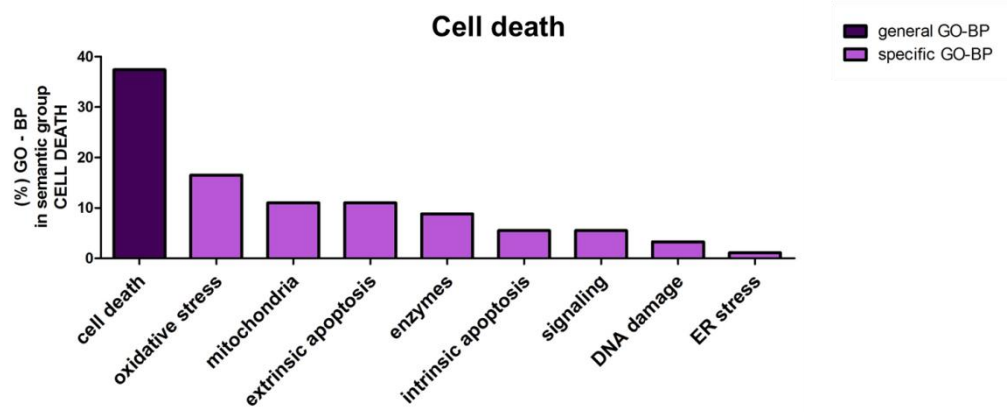
Semantic classes	Number of Terms	%
ADHESION		**%**
adhesion	*8*	***32.0***
cell-cell	6	**24.0**
cell-substrate	5	**20.0**
adherens-junction	4	**16.0**
cell-matrix	2	**8.0**
total	**25**	**100**

Supporting Figure S29



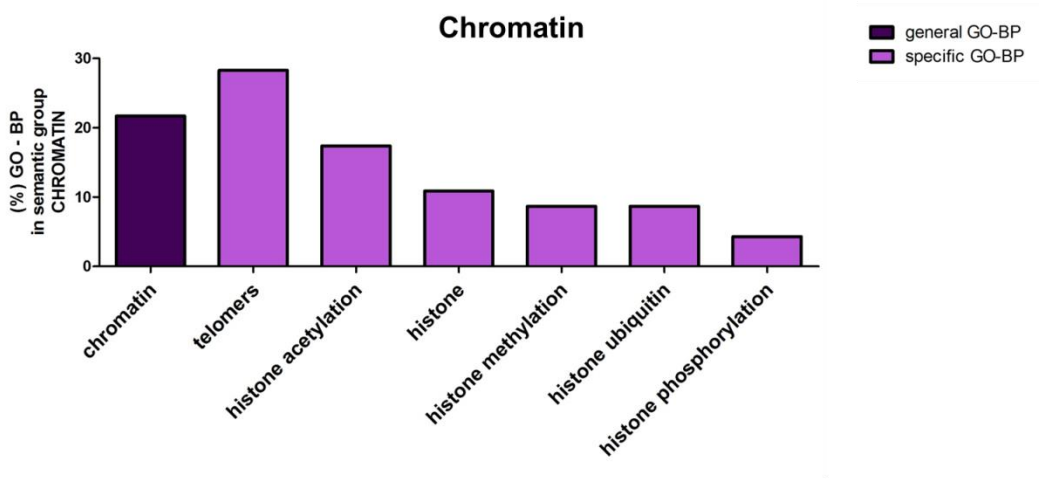
CELL CYCLE		%
cell cycle	20	**17.9**
segregation/cytokinesis	21	**18.8**
mitotic phase transition	13	**11.6**
cytoskeleton	13	**11.6**
DNA - damage checkpoint	12	**10.7**
G1/S phase transition	9	**8.0**
enzymes	6	**5.4**
checkpoint	5	**4.5**
G2/M phase transition	4	**3.6**
DNA - damage checkpoint G1	4	**3.6**
ubiquitin-proteasome	4	**3.6**
DNA - damage checkpoint G2	1	**0.9**
total	**112**	**100.0**

Supporting Figure S30



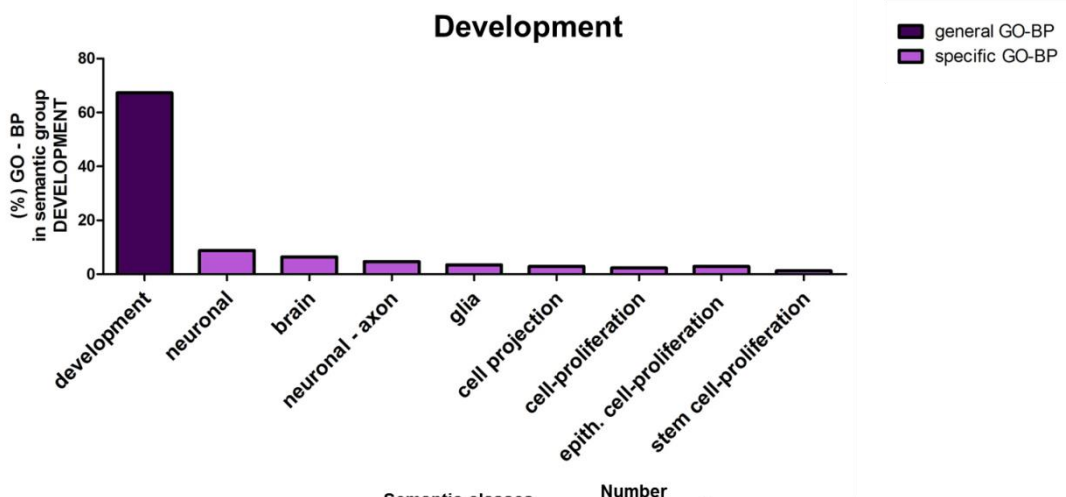
Semantic classes	Number of Terms	%
CELL DEATH		**%**
cell death	34	**37.4**
oxidative stress	15	**16.5**
mitochondria	10	**11.0**
extrinsic apoptosis	10	**11.0**
enzymes	8	**8.8**
intrinsic apoptosis	5	**5.5**
signaling	5	**5.5**
DNA damage	3	**3.3**
ER stress	1	**1.1**
total	**91**	**100**

Supporting Figure S31



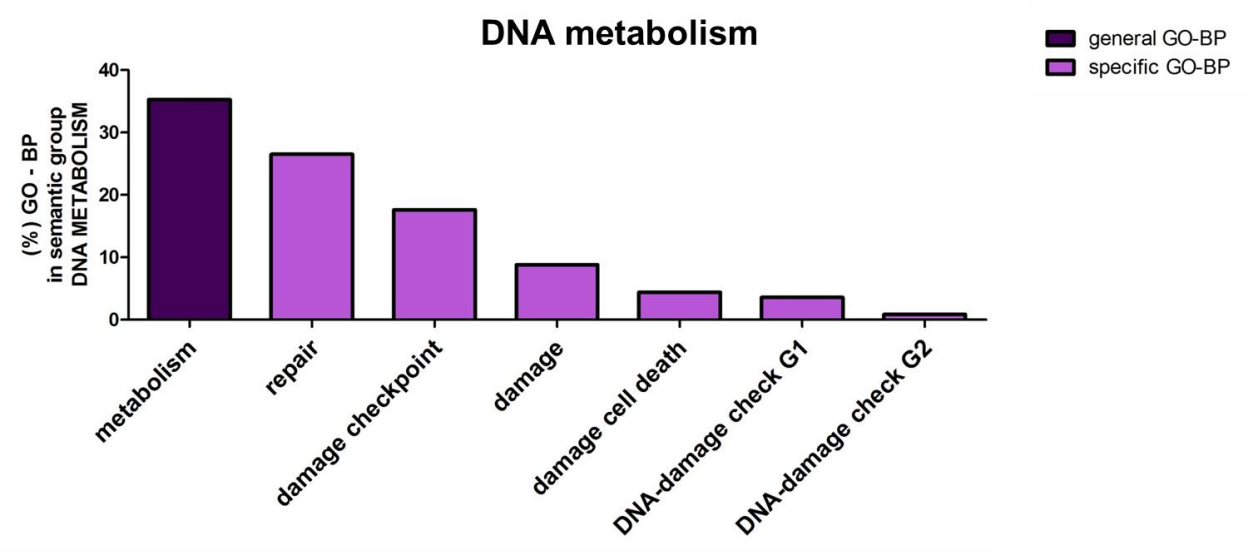
Semantic classes	Number of Terms	%
CHROMATIN		**%**
chromatin	10	**21.7**
telomers	13	**28.3**
histone - acetylation	8	**17.4**
histone	5	**10.9**
histone - methylation	4	**8.7**
histone ubiquitin	4	**8.7**
histone - phosphorylation	2	**4.3**
total	**46**	**100.0**

Supporting Figure S32



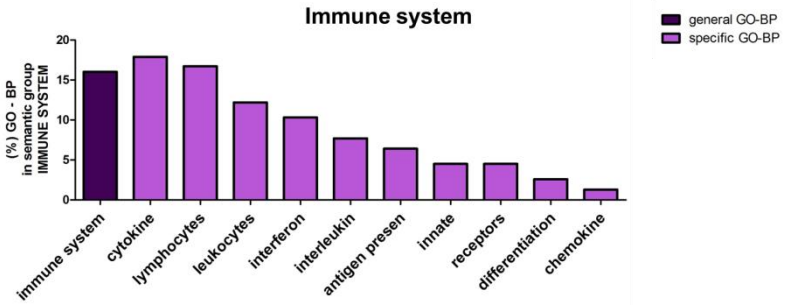
Semantic classes	Number of Terms	%
DEVELOPMENT		**%**
development	115	**67.3**
neuronal	15	**8.8**
brain	11	**6.4**
neuronal - axon	8	**4.7**
glia	6	**3.5**
cell projection	5	**2.9**
cell-proliferation	4	**2.3**
epith. cell-proliferation	5	**2.9**
stem cell-proliferation	2	**1.2**
total	**171**	**100**

Supporting Figure S33



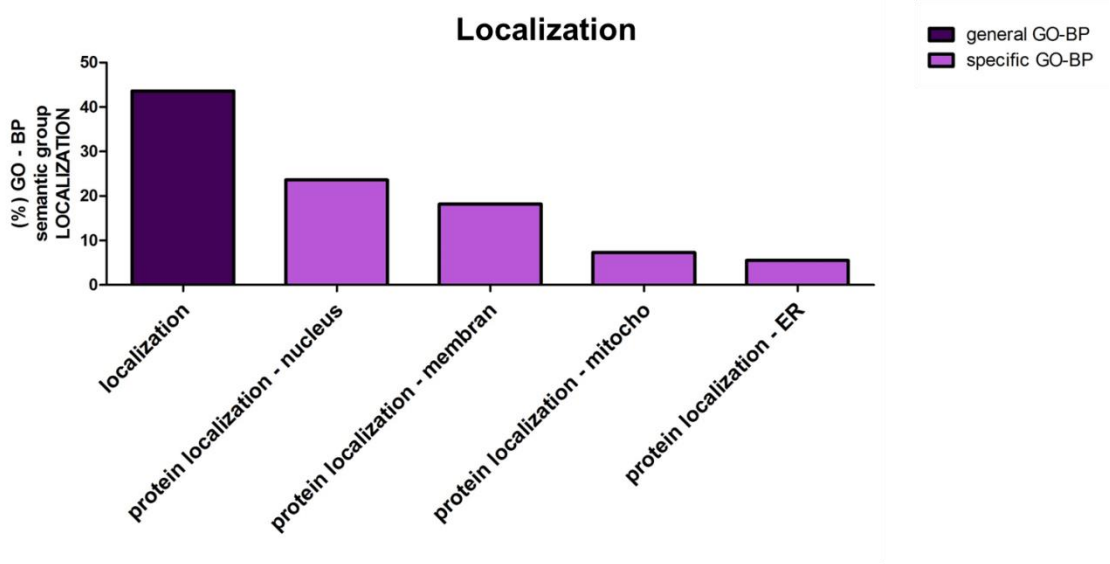
Semantic classes	Number of Terms	%
DNA METABOLISM		**%**
metabolism	24	**35.3**
repair	18	**26.5**
DNA - damage checkpoint	12	**17.6**
damage	6	**8.8**
DNA - damage checkpoint G1	4	**5.9**
damage cell death	3	**4.4**
DNA - damage checkpoint G2	1	**1.5**
total	**68**	**100.0**

Supporting Figure S34



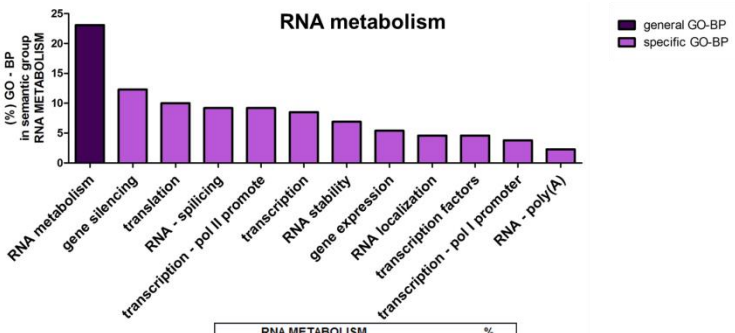
Semantic classes	Number of Terms	%
IMMUNE SYSTEM		**%**
immune system	25	**16.0**
cytokine	28	**17.9**
lymphocytes	26	**16.7**
leukocytes	19	**12.2**
interferon	16	**10.3**
interleukin	12	**7.7**
antigen presentation	10	**6.4**
innate	7	**4.5**
receptors	7	**4.5**
differentiation	4	**2.6**
chemokine	2	**1.3**
total	**156**	**100**

Supporting Figure S35



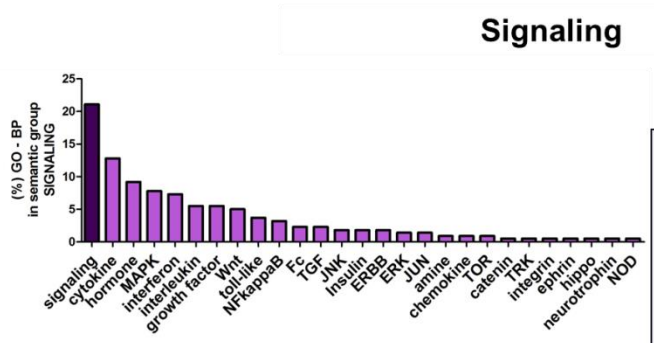
Semantic classes	Number of Terms	%
LOCALIZATION		**%**
localization	24	**44.4**
protein localization - nucleus	13	**24.1**
protein localization - membrane	10	**18.5**
protein localization - mitochondria	4	**7.4**
protein localization - ER	3	**5.6**
total	**54**	**100.0**

Supporting Figure S36



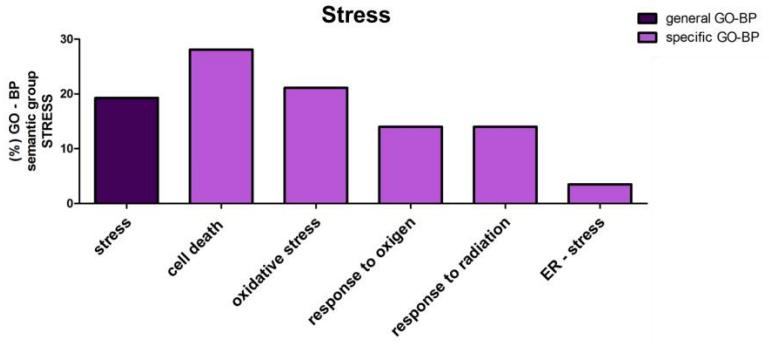
RNA METABOLISM		%
RNA - metabolism	30	**23.1**
gene silencing	16	**12.3**
translation	13	**10.0**
RNA - spilicing	12	**9.2**
transcription - pol II promoter	12	**9.2**
transcription	11	**8.5**
RNA stability	9	**6.9**
gene expression	7	**5.4**
transcription factors	6	**4.6**
RNA - localization	6	**4.6**
transcription - pol I promoter	5	**3.8**
RNA - poly(A)	3	**2.3**
total	**130**	**100.0**

Supporting Figure S37



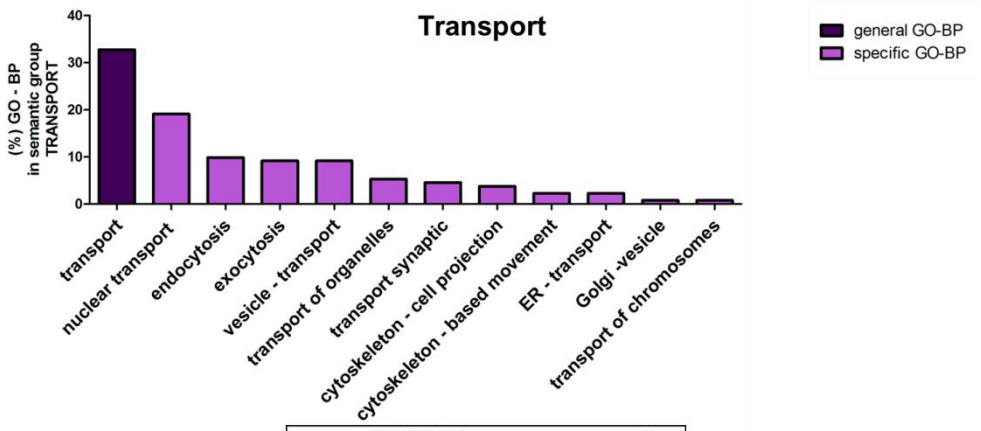
Semantic classes	Number of Terms	%
SIGNALING		**%**
signaling	46	**21.1**
cytokine	28	**12.8**
hormone	20	**9.2**
MAPK	17	**7.8**
interferon	16	**7.3**
growth factor	12	**5.5**
interleukin	12	**5.5**
Wnt	11	**5.0**
toll-like	8	**3.7**
NFkappaB	7	**3.2**
TGF	5	**2.3**
Fc	5	**2.3**
ERBB	4	**1.8**
insulin	4	**1.8**
JNK	4	**1.8**
ERK	3	**1.4**
JUN	3	**1.4**
amine	2	**0.9**
TOR	2	**0.9**
chemokine	2	**0.9**
catenin	1	**0.5**
ephrin	1	**0.5**
hippo	1	**0.5**
integrin	1	**0.5**
neurotrophin	1	**0.5**
NOD	1	**0.5**
TRK	1	**0.5**
total	**218**	**100.0**

Supporting Figure S38



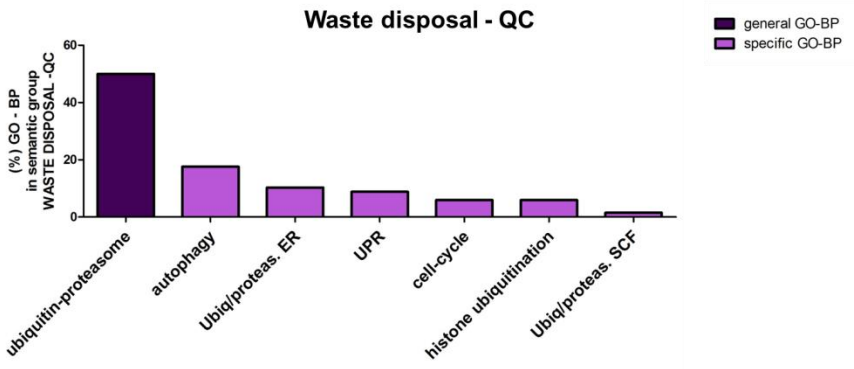
Semantic classes	Number of Terms	%
STRESS		**%**
stress	11	**19.3**
cell death	16	**28.1**
response to oxigen	8	**14.0**
response to radiation	8	**14.0**
oxidative stress	12	**21.1**
ER - stress	2	**3.5**
total	**57**	**100.0**

Supporting Figure S39



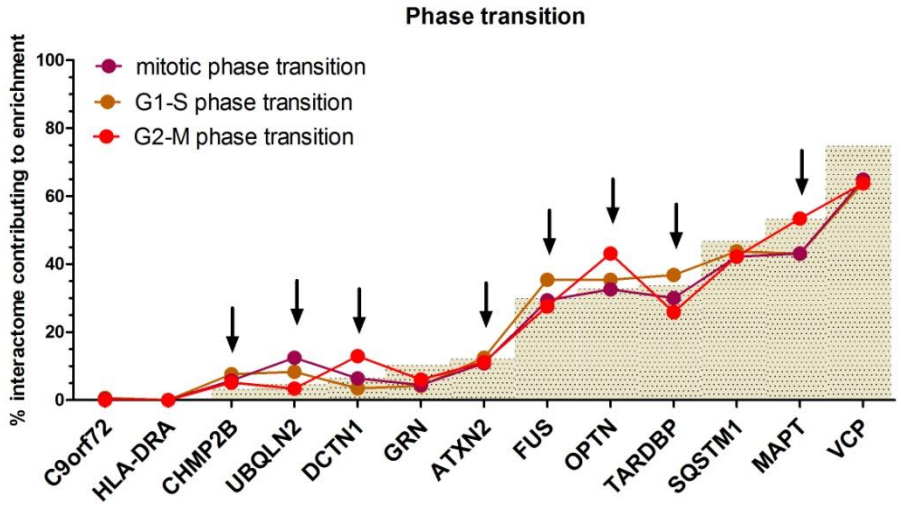
TRANSPORT		%
transport	43	**32.8**
nuclear transport	25	**19.1**
endocytosis	13	**9.9**
exocytosis	12	**9.2**
vesicle - transport	12	**9.2**
transport of organelles	7	**5.3**
transport synaptic	6	**4.6**
cytoskeleton - cell projection	5	**3.8**
ER - transport	3	**2.3**
cytoskeleton - based movement	3	**2.3**
Golgi -vesicle	1	**0.8**
transport of chromosomes	1	**0.8**
total	**131**	**100.0**

Supporting Figure S40

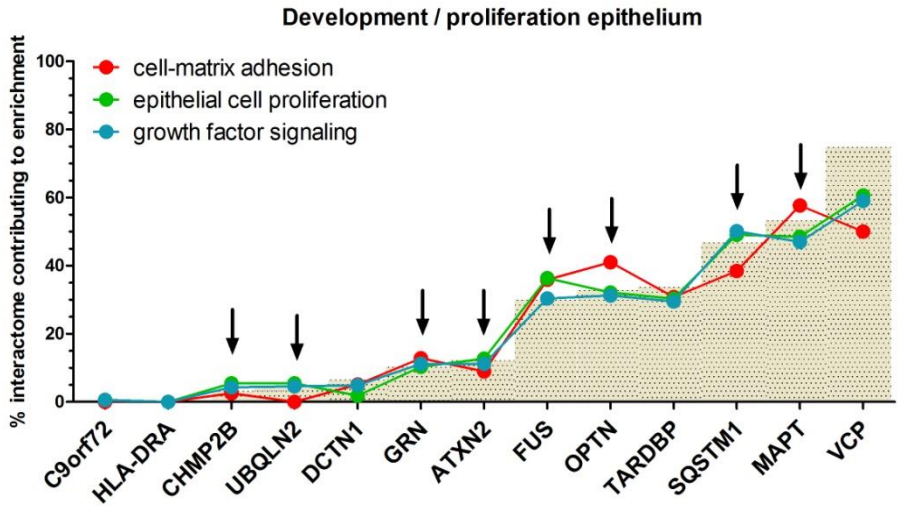


Semantic classes	Number of Terms	%
WASTE DISPOSAL-QC		%
ubiquitin-proteasome	34	**50.0**
autophagy	12	**17.6**
ubiquitin-proteasome - ER	7	**10.3**
UPR	6	**8.8**
cell cycle	4	**5.9**
histone ubiquitination	4	**5.9**
ubiquitin-proteasome - SCF	1	**1.5**
total	**68**	**100.0**

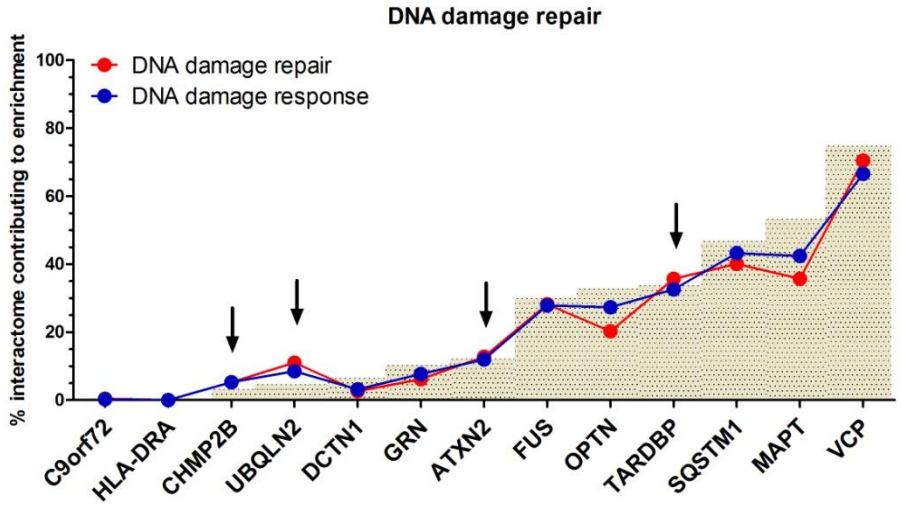
Supporting Figure S41



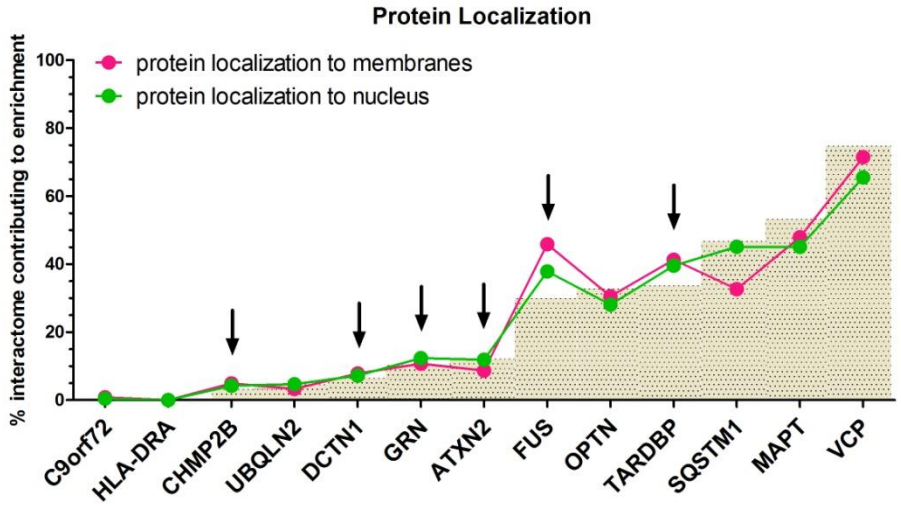
Supporting Figure S42



Supporting Figure S43



Supporting Figure S44



Supporting Figure S45

	ATXN2	DCT1N	FUS	GRN	MAPT	OPTN	SQSTM1	TARDBP	UBQLN2	VCP
intrinsic apoptosis after DNA damage	23.8	4.8	31.7	11.1	54.0	39.7	52.4	41.3	9.5	68.3
DNA damage checkpoint	12.0	5.6	30.4	4.0	44.8	35.2	44.8	32.8	5.6	69.6
cell cycle checkpoint	11.2	4.8	29.6	4.0	42.4	32.8	42.4	32.8	5.6	71.2
DNA damage checkpoint G1	20.0	2.2	35.6	6.7	60.0	55.6	57.8	33.3	8.9	68.9
DNA damage response	11.9	3.2	27.9	7.7	42.4	27.3	43.2	32.6	8.5	66.6
apoptotic signaling	11.6	6.3	29.5	10.3	51.7	36.7	56.4	35.4	5.0	65.5
cell death intrinsic apoptosis	16.0	6.1	30.1	14.1	51.5	33.7	52.8	37.4	7.4	71.8
mitotic phase transition	10.9	6.4	29.4	4.5	43.1	32.6	42.2	30.0	12.5	64.9
G2-M phase transition	11.2	12.9	27.6	6.0	53.4	43.1	42.2	25.9	3.4	63.8
G1-S phase transition	12.5	3.5	35.4	4.2	43.1	35.4	43.8	36.8	8.3	63.9
DNA damage repair	12.8	2.6	28.2	6.2	35.7	20.3	40.1	35.7	11.0	70.5
epithelial cell proliferation	12.7	1.8	36.4	10.3	48.5	32.1	49.1	30.3	5.5	60.6
cell-matrix adhesion	9.0	5.1	35.9	12.8	57.7	41.0	38.5	30.8	0.0	50.0
growth factor signaling	11.2	4.9	30.4	11.2	47.0	31.2	50.1	29.5	4.6	59.0
ER transport	4.0	8.0	8.0	16.0	28.0	8.0	36.0	44.0	16.0	96.0
ER stress	8.8	6.8	22.3	13.5	41.2	20.9	46.6	37.8	16.9	81.8
ER ubiquitin-proteasome	6.2	5.3	17.7	13.3	36.3	18.6	43.4	38.1	18.6	83.2
UPR	11.2	9.2	28.6	25.5	50.0	22.4	46.9	41.8	11.2	78.6
response to oxidative stress	18.6	7.2	34.7	12.6	51.5	29.9	54.5	38.3	7.8	65.9
response to ionizing radiation	9.7	3.1	30.1	8.7	39.8	27.6	45.9	35.2	5.1	68.9
gene expression	10.1	3.4	31.6	6.6	37.5	22.2	36.6	30.9	3.6	57.9
translation	10.9	3.0	43.9	2.8	44.4	15.5	27.9	41.1	1.5	66.5
transcription	10.8	3.1	29.6	8.4	35.6	24.3	40.3	27.7	3.6	58.0
transcription-RNA pol II	12.5	2.8	32.1	8.7	33.8	21.4	41.4	27.1	4.3	58.0
protein localization to membrane	8.7	7.9	45.9	10.7	47.9	30.6	32.6	41.3	3.3	71.5
protein localization to nucleus	11.9	7.2	37.9	12.3	45.1	28.1	45.1	39.6	4.7	65.5